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(54) Title: A PROCESS FOR THE PREPARATION OF LIPASE (57) Abstract A process for producing an active lipase enzyme <i>in vitro</i> , comprising mixing an inactive or partly active lipase enzyme with a chaperone molecule and subjecting the mixture to denaturation followed by renaturation to produce the active lipase enzyme.		

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A PROCESS FOR THE PREPARATION OF LIPASE

FIELD OF INVENTION

The present invention relates to processes for preparing an active lipase enzyme in vitro, a DNA construct encoding the lipase, a recombinant vector including the DNA construct, as well as a host cell transformed with the vector.

BACKGROUND OF THE INVENTION

Lipases are enzymes which catalyze the hydrolysis of ester bonds in triglycerides resulting in the formation of diglycerides, monoglycerides, glycerin and free fatty acids. Some lipases also catalyze other reactions involving ester bonds such as
10 synthesis of ester bonds or transesterification reactions. Lipases are produced by a wide variety of different organisms. Microbial lipases in particular are of considerable practical utility for a variety of purposes where lipolysis of fats is desired, e.g. in the food industry and in detergents.

One particular lipase which has been found to be particularly advantageous for
15 inclusion in a detergent for the removal of fatty stains or soiling from fabrics is a lipase produced by strains of Pseudomonas cepacia. In EP 214 761 (to Novo Industri A/S), this lipase is disclosed as a lipase which is active at a temperature below 60°C, which is important as most present-day fabrics are washed at temperatures below 60°C.

20 Another important Pseudomonas cepacia lipase for use as a detergent additive is the one disclosed in WO 89/01032 (to Novo Industri A/S) as a positionally non-specific lipase, i.e. one which is able to react with all three fatty acyl groups of a triglyceride.

In order to facilitate Pseudomonas cepacia lipase production, it may be
25 advantageous to employ recombinant DNA techniques, for instance in order to

optimize lipase expression by introducing a stronger promoter from which the DNA sequence encoding the enzyme is expressed or by introducing more efficient ribosome binding sites or signal peptide coding sequences, or in order to select a host organism for the production of the enzyme which is easier to cultivate (e.g. in terms of its being a standard production organism such as E. coli or the like) or which results in higher lipase yields.

However, as described below, such approaches will sometimes fail to yield the expected results, e.g. in cases where one or more genes in addition to the structural gene coding for the protein in question, play some part in the production of the gene product (examples of such genes are the Bacillus sac and iep genes, and genes required for the production of Klebsiella pullulanase and E. coli hemolysin).

The cloning of a lipase gene from another Pseudomonas species, Pseudomonas fragi, is known from, e.g., S. Aoyama et al. (1988) and W. Kugimiya et al. (1986). However, the lipase produced by P. fragi differs from that of P. cepacia in its amino acid sequence, and in these publications, there is no indication that one or more additional genes may be required in order to achieve a significant lipase production in a host organism.

EP 331 376 discloses a recombinant DNA encoding a Pseudomonas cepacia lipase as well as a protein participating in the production of the lipase.

WO 90/00908 discloses the production of a Pseudomonas cepacia lipase in heterologous host cells by means of a polypeptide expressed in the host cell, which polypeptide acts as a modulator of lipase production.

SUMMARY OF THE INVENTION

It has surprisingly been found possible to increase the yield of an active lipase enzyme produced by a recombinant host cell when the lipase recovered from the

cells is subjected to denaturation followed by renaturation in the presence of a chaperone molecule.

Accordingly, the present invention relates to a process for preparing an active lipase enzyme in vitro, the process comprising

- 5 (a) culturing a host cell transformed with a DNA sequence encoding a lipase enzyme under suitable conditions to produce the lipase enzyme in inactive or partly active form, recovering the lipase enzyme from the culture, and subjecting the recovered lipase enzyme to denaturation,
- (b) mixing the denaturated lipase enzyme with a chaperone molecule, and
- 10 (c) subjecting the mixture of step (b) to renaturation to produce the active lipase enzyme.

Alternatively, the invention relates to a process for preparing an active lipase enzyme in vitro, the process comprising

- (a) culturing a host cell transformed with a DNA sequence encoding a lipase enzyme
- 15 under suitable conditions to produce the lipase enzyme in inactive or partly active form and recovering the lipase enzyme from the culture,
- (b) mixing the recovered lipase enzyme with a chaperone molecule, and
- (c) subjecting the mixture of step (b) to denaturation followed by renaturation to produce the active lipase enzyme.

- 20 In a further embodiment, the invention relates to a process for preparing an active lipase enzyme in vitro, the process comprising

- (a) culturing a host cell transformed with a DNA sequence encoding a lipase enzyme and with a DNA sequence encoding a chaperone molecule under suitable conditions to produce the lipase enzyme in inactive or partly active form and recovering a lipase enzyme chaperone molecule mixture from the culture, and
- 5 (b) subjecting the mixture of step (a) to denaturation followed by renaturation to produce the active lipase enzyme, optionally with addition of a further amount of chaperone molecule to the mixture.

As indicated above, the present invention is based on the finding that the natural conformation of a protein or protein complex is not always only determined by the
10 amino acid sequence of the protein. Thus, in some cases, accessory proteins, termed chaperone molecules, are required to mediate the formation of the correct tertiary structure of another protein or protein complex, but are not themselves components of the final functional structure (Ellis et al., 1991).

In the present context, the term "chaperone molecule" is intended to indicate such
15 accessory proteins, i.e. a protein involved in facilitating other polypeptides in maintaining the unfolded state, enabling their correct transmembrane targeting or folding and oligomeric assembly, and in disassembly of protein complexes (cf. R.J. Ellis and S.M. Hemmingsen (1989), J.E. Rothman (1989), Morimoto et al.(1990)). Although, in general, a covalent modification of the target protein or protein complex
20 has not been observed by the action of a chaperone molecule it cannot be excluded that the chaperone molecule to be used in the processes of the invention is capable of causing such covalent modification. Accordingly, the term "chaperone molecule" as used herein is intended to include a chaperone molecule causing non-covalent as well as covalent modification of the lipase enzyme.

25 In another aspect, the present invention relates to a DNA construct comprising a first DNA sequence encoding a lipase enzyme fused to a second DNA sequence encoding a chaperone molecule in such a way that the lipase enzyme and

chaperone molecule or functional part thereof are expressed as a single fusion protein on culturing a suitable host cell transformed with the DNA construct.

DETAILED DISCLOSURE OF THE INVENTION

The chaperone molecule to be added to the recovered and optionally denaturated lipase enzyme in step b) above is advantageously produced by a process comprising culturing a host cell transformed with a DNA sequence encoding a chaperone molecule under suitable conditions to produce the chaperone molecule and recovering the chaperone molecule from the culture. Furthermore, when the chaperone molecule is to be added to a denaturated lipase enzyme it may be advantageous that the chaperone molecule itself is denaturated. Accordingly, the process of the invention may comprise a further step in which the chaperone molecule is subjected to a denaturation treatment before it is mixed with the denaturated lipase enzyme in step b).

In the present context, "partly active form" as used about the lipase enzyme is intended to indicate that the lipase has some, but not full activity as determined by an activity measurement, e.g. by titration using a pH stat as later described. Less than full activity is taken to mean, that the partly active lipase preparation has a lower specific activity than a corresponding preparation of fully active lipase protein, the two preparations containing the same total amount of lipase protein.

The denaturation of the inactive or partly active lipase enzyme and optionally the chaperone molecule, which may be performed separately or on a mixture of the two components according to the processes of the invention may be carried out in a manner known per se. For instance, the denaturation may be obtained by subjecting the mixture to the action of a denaturing agent (e.g. 8M urea) and subsequently removing this agent, e.g. by dialysis.

Preferred lipases for production by the process of the invention are lipases derived from a Pseudomonas sp. or a Chromobacter sp. In particular, the lipase enzyme

may be a Pseudomonas cepacia, Pseudomonas fragi, Pseudomonas gladioli,
Pseudomonas fluorescens, Pseudomonas stutzeri, Pseudomonas alcaligenes,
Pseudomonas pseudoalcaligenes, Pseudomonas putida, Pseudomonas glumae (e.g.
as described in EP 407 225), Pseudomonas aeruginosa or Chromobacter viscosum
5 lipase, or a derivative of said lipase enzyme. In particular, the lipase enzyme is one
derived from a strain of Pseudomonas cepacia, e.g. a strain deposited in the Deut-
sche Sammlung von Mikroorganismen in connection with the invention disclosed in
EP 214 761, with the deposit numbers DSM 3333-3337 and DSM 3401, as well as
the strain deposited in the Deutsche Sammlung von Mikroorganismen in connection
10 with the invention disclosed in WO 89/01032, with the deposit number DSM 3959.

In the present context, the term "derivative" is intended to indicate a protein with
lipolytic activity which is derived from the native lipase by suitably modifying the DNA
sequence coding for the native lipase, resulting in the addition of one or more amino
acids to either or both the C- and N-terminal end of the native protein, substitution
15 of one or more amino acids at one or a number of different sites in the native amino
acid sequence, deletion of one or more amino acids at either or both ends of the
native protein or at one or more sites in the amino acid sequence, or insertion of one
or more amino acids at one or more sites in the native amino acid sequence. Such
modifications of DNA coding for native proteins are well known and widely practised
20 in the art. Typically, the amino acid sequence of the derivative will be homologous
to that of the native lipase protein, e.g. exhibiting a substantial degree of homology,
or the derivative will react with an antibody raised against the native lipase.

The host cell used in the process of the invention may be any suitable bacterium
which, on cultivation, produces large amounts of the lipase. Examples of suitable
25 bacteria may be grampositive bacteria such as Bacillus subtilis, Bacillus licheniformis,
Bacillus lentus, Bacillus brevis, Bacillus stearothermophilus, Bacillus alkalophilus,
Bacillus amyloliquefaciens, Bacillus coagulans, Bacillus circulans, Bacillus lautus or
Streptomyces lividans. It has been found that E. coli is able to produce a high yield,
i.e. at least 5% of the total cellular protein, of (intracellular) lipase, and is therefore
30 a preferred host organism. In E. coli, the lipase enzyme is typically produced in the

form of inclusion bodies. The transformation of the bacteria may for instance be effected by protoplast transformation or by using competent cells in a manner known per se. Another suitable bacterial host cell is a cell of a Pseudomonas spp. such as Pseudomonas cepacia, Pseudomonas fragi, Pseudomonas gladioli, Pseudomonas fluorescens, Pseudomonas stutzeri, Pseudomonas alcaligenes, Pseudomonas pseudoalcaligenes, Pseudomonas putida, Pseudomonas glumae or Pseudomonas aeruginosa.

Alternatively, the host cell may be a fungus, i.e. a cell of a yeast or of a filamentous fungus. The yeast host cell may, for instance, be a cell of the genus Saccharomyces such as S. cerevisiae. The filamentous fungus host organism may conveniently be one which has previously been used as a host for producing recombinant proteins, e.g. a strain of Aspergillus sp., such as A. niger, A. nidulans or A. oryzae. The techniques used to transform a fungal host cell and obtain expression of the recombinant protein may suitably be as described in EP 238 023.

15 For expression of the protein in the host cell the DNA sequence encoding the protein may be preceded by a promoter. The promoter may be any DNA sequence exhibiting a strong transcriptional activity in the host cell of choice and may be derived from a gene encoding an extracellular or intracellular protein such as an amylase, a glucoamylase, a protease, a lipase, a cellulase or a glycolytic enzyme.

20 Other sequences involved in expression of the protein include termination and polyadenylation sequences as well as ribosome binding sites and may suitably be derived from the same sources as the promoter.

In the process of the invention, the DNA sequence encoding the lipase enzyme and/or the chaperone molecule is advantageously preceded by the promoter of the 25 Bacillus stearothermophilus maltogenic amylase gene, Bacillus licheniformis α -amylase gene, Bacillus amyloliquefaciens α -amylase gene, Bacillus subtilis alkaline protease gene, or Bacillus pumilus xylosidase gene, or by the phage Lambda P_R or P_L promoters, the phage T7 gene 10 promoter or the E. coli *lac* promoter. The DNA

sequence encoding the lipase enzyme and/or the chaperone molecule may be preceded by a ribosome binding site of the Bacillus stearothermophilus maltogenic amylase gene, Bacillus licheniformis α -amylase gene, Bacillus amyloliquefaciens α -amylase gene, Bacillus subtilis alkaline protease gene, Bacillus pumilus xylosidase 5 gene, phage T7 gene 10 or E. coli *lac* gene.

According to the invention, the chaperone molecule is advantageously a Pseudomonas lipase modulator protein, preferably selected from the group consisting of the Pseudomonas cepacia lipase modulator (disclosed in WO 90/00908), the Pseudomonas glumae lipase modulator, and the Pseudomonas 10 aeruginosa lipase modulator, or a derivative of any such lipase modulator.

In the present context, a derivative of a lipase modulator is to be understood in the same manner as indicated above in connection with derivatives of the lipase enzyme, i.e. a protein with chaperone activity which is derived from the native lipase by suitably modifying the DNA sequence coding for the native lipase modulator as 15 discussed above. The chaperone activity of the derivative may, for instance, be determined by analysing the capability of the derivative in producing an active lipase enzyme as explained herein.

In a preferred embodiment of the process according to the invention, the lipase enzyme is a Pseudomonas cepacia lipase or a derivative thereof, and the chaperone 20 molecule is a Pseudomonas cepacia lipase modulator (or a derivative thereof) (both disclosed in WO 90/00908).

The DNA construct of the invention comprising the DNA sequence encoding the lipase enzyme and/or the chaperone molecule may be of genomic or cDNA origin, for instance obtained by preparing a genomic or cDNA library of an appropriate 25 organism, and screening for DNA sequences coding for all or part of the lipase or the chaperone by hybridization using synthetic oligonucleotide probes in accordance with standard techniques (cf. Sambrook et al., 1989).

The DNA construct of the invention may also be prepared synthetically by established standard methods, e.g. the phosphoramidite method described by S.L. Beaucage et al. (1981), Matthes et al. (1984). According to the phosphoramidite method, oligonucleotides are synthesized, e.g. in an automatic DNA synthesizer, 5 purified, ligated, and cloned in an appropriate vector.

Finally, the DNA construct may be of mixed synthetic and genomic, mixed synthetic and cDNA or mixed genomic and cDNA origin prepared by ligating fragments of synthetic, genomic or cDNA origin (as appropriate), the fragments corresponding to various parts of the entire DNA construct, in accordance with standard 10 techniques.

In the DNA construct of the invention, the DNA sequence encoding the lipase enzyme may be one derived from a Pseudomonas sp. or a Chromobacter sp. For instance, the first DNA sequence may be one encoding a Pseudomonas cepacia, Pseudomonas fragi, Pseudomonas gladioli, Pseudomonas fluorescens, 15 Pseudomonas stutzeri, Pseudomonas alcaligenes, Pseudomonas pseudoalcaligenes, Pseudomonas putida, Pseudomonas glumae, Pseudomonas aeruginosa or Chromobacter viscosum lipase, or a derivative of said lipase enzyme. The second DNA sequence may be one encoding a Pseudomonas cepacia lipase modulator, a Pseudomonas glumae lipase modulator, a Pseudomonas aeruginosa lipase 20 modulator, or another Pseudomonas lipase modulator protein or a derivative of any of these modulators. Most preferably, the first DNA sequence encodes a Pseudomonas cepacia lipase or a derivative thereof, and the second DNA sequence encodes a Pseudomonas cepacia lipase modulator or a derivative thereof, as described in WO 90/00908 incorporated herein by reference.

25 A particularly preferred DNA construct is one which has the sequence shown in the SEQ ID No. 5 appended hereto. The sequence may be modified in accordance with conventional practise. Examples of suitable modifications of the DNA sequence are nucleotide substitutions which do not give rise to another amino acid sequence of the lipase or lipase modulator, but which may correspond to the codon usage of the

host organism into which the DNA construct is introduced or nucleotide substitutions which do give rise to a different amino acid sequence and therefore, possibly, a different polypeptide structure without, however, impairing the properties of either the lipase or the lipase modulator. Other examples of possible modifications are insertion
5 of one or more nucleotides into the sequence, addition of one or more nucleotides at either end of the sequence and deletion of one or more nucleotides at either end of or within the sequence.

In a further aspect, the invention relates to a recombinant expression vector comprising a DNA construct as described above. The expression vector carrying the
10 DNA sequence encoding the lipase and/or chaperone molecule may be any vector which is capable of replicating autonomously in a given host organism, typically a plasmid or bacteriophage. In the vector, the DNA sequence encoding the lipase and/or chaperone molecule should be operably connected to a suitable promoter sequence. The promoter may be any DNA sequence which shows transcriptional
15 activity in the host cell and may be derived from genes encoding proteins either homologous or heterologous to the host organism. The promoter is preferably the promoter of the Bacillus stearothermophilus maltogenic amylase gene, Bacillus licheniformis α -amylase gene, Bacillus amyloliquefaciens α -amylase gene, Bacillus subtilis alkaline protease gene, or Bacillus pumilus xylosidase gene, or by the phage
20 Lambda P_R or P_L promoters, the phage T7 gene 10 promoter or the E. coli *lac* promoter.

The vector may also comprise a selectable marker, e.g. a gene whose product confers antibiotic resistance, such as ampicillin, chloramphenicol or tetracycline resistance, or the dal genes from B. subtilis or B. licheniformis.

25

In a still further aspect, the present invention relates to a process for preparing a lipase in active form, the process comprising culturing a host cell transformed with the DNA construct described above under suitable conditions to produce the lipase, and recovering the lipase from the culture, optionally followed by denaturation and
30 renaturation of the lipase/chaperone fusion protein.

The medium used to cultivate the cells may be any conventional medium suitable for growing bacteria. The lipase may be recovered from the medium by conventional procedures including separating the cells from the medium by centrifugation or filtration, if necessary after disruption of the cells to recover an intracellular product, 5 precipitating the proteinaceous components of the supernatant or filtrate by means of a salt, e.g. ammonium sulphate, followed by purification by a variety of chromatographic procedures, e.g. ion exchange chromatography, affinity chromatography, or the like.

While the use of chaperone molecules in the preparation of active lipase enzyme is 10 considered to be of particular importance in connection with recombinant DNA techniques (as explained above), it is believed that the presence of a chaperone molecule is critical in connection with any denaturation and renaturation treatment in which an active lipase enzyme, as described herein, is desired, irrespective of the production method of the lipase enzyme. Thus, for instance in connection with 15 a lipase enzyme produced by conventional fermentation of a naturally-occurring or non-genetically engineered organism, which is to be subjected to a denaturation treatment, it is believed that the presence of a chaperone molecule in the subsequent renaturation treatment is critical.

Accordingly, in a further general aspect the invention relates to a process for 20 denaturing and renaturing a lipase enzyme, the process comprising

- (a) subjecting a lipase enzyme to a denaturation treatment,
- (b) mixing the denaturated lipase enzyme obtained in step (a) with a chaperone molecule which has optionally been subjected to a denaturation treatment, and
- (c) subjecting the mixture of step (b) to renaturation to produce the active lipase 25 enzyme.

Alternatively, the denaturation/renaturation treatment of the lipase enzyme may be carried out by

- a) mixing a lipase enzyme to be subjected to the denaturation and renaturation treatment with a chaperone molecule, and
- 5 b) subjecting the mixture of step a) to denaturation followed by renaturation so as to produce an active lipase enzyme.

DESCRIPTION OF THE DRAWINGS

The present invention is described in the following with reference to the appended drawings, in which

10 Fig. 1 illustrates the plasmid pAHE2;

Fig. 2 illustrates the plasmid pAHE8;

Fig. 3 illustrates the plasmid pAHE10;

Fig. 4 illustrates the plasmid pCBE6;

Fig. 5 illustrates the plasmid pCBE7;

15 Fig. 6 illustrates the plasmid pCBE12;

Fig. 7 illustrates the plasmid pCBE18;

Fig. 8 illustrates the plasmid pCBE19;

Fig. 9 shows the result of a SDS-PAGE analysis of proteins expressed in E. coli JA221 performed as described in Example 3, in which lanes:

A & S	molecular weight markers; 45, 36, 24 and 20		
B	pJW2 (vector)		
C	pSJ150 (original lipase construct in pUC)		
D	pAHE2	30°C	1.0 hours(hr)
5 E	pAHE2	42°C	1.0 hrs
F	pAHE2	42°C	1.5 hrs
G	pAHE2	42°C	2.0 hrs
H, M & R	purified lipase from <u>P. cepacia</u>		
I	pAHE10	30°C	1.0 hrs
10 J	pAHE10	42°C	1.0 hrs
K	pAHE10	42°C	1.5 hrs
L	pAHE2	42°C	2.0 hrs
N	pCBE6	-IPTG	1.0 hrs
O	pCBE6	+IPTG	1.0 hrs
15 P	pCBE6	+IPTG	1.5 hrs
Q	pCBE6	+IPTG	2.0 hrs

Fig. 10 shows the result of an immunoblot analysis performed as described in Example 3 using Lip antibody, in which lanes:

A	pJW2 (vector)		
20 B	pSJ150		
C	pAHE2	30°C	1.0 hr
D	pAHE2	42°C	1.0 hr
E	pAHE2	42°C	1.5 hrs
F	pAHE2	42°C	2.0 hrs
25 G,L,Q,S	purified lipase from <u>P. cepacia</u> (10LU)		
H	pAHE10	30°C	1.0 hr
I	pAHE10	42°C	1.0 hr
J	pAHE10	42°C	1.5 hrs
K	pAHE10	42°C	2.0 hrs
30 M	pCBE6	-IPTG	1.0 hr

N	pCBE6	+IPTG	1.0 hr
O	pCBE6	+IPTG	1.5 hrs
P	pCBE6	+IPTG	2.0 hrs
R	pAHE2 + pAHE10, 42°C 1.5 hrs;		

5 Fig. 11 illustrates the cellular localization of LimA in P. cepacia as determined by an immunoblot analysis of lipase (Fig. 11a) and Lim (Fig. 11b) induced with oleyl alcohol in intracellular (cytoplasm and inner cell membrane), periplasmic and extracellular fractions of P. cepacia (Example 7). Equal amounts of protein were loaded in each lane corresponding to 0.01, 17 and 21%, respectively. In (a) (Lipase

10 immunoblot) the lanes contained:

- A purified lipase from P. cepacia
- B intracellular fraction
- C periplasmic fraction
- D extracellular fraction,

15 in (b) (Lim immunoblot) the lanes contained:

- A lim expressed from pJ38
- B intracellular fraction
- C periplasmic fraction
- D extracellular fraction;

20 Fig. 12 illustrates the plasmid pAHE19;

Fig. 13 illustrates the plasmid pAHE22;

Fig. 14 illustrates the plasmid pAHE16;

Fig. 15 illustrates the plasmid pAHE23; and

Fig. 16 illustrates the plasmid pCBF1-6.

The present invention is further illustrated in the following examples which are not in any way intended to limit the scope of the invention as claimed.

MATERIALS AND METHODS

Bacterial Strains

5 E. coli TG1 supE hsd-5 thi-(lac-proAB) F'[traD36proAB+lacIq lacZ-M15) (Gibson, 1984)

E. coli JA221 (Clarke and Carbon, 1978)

E. coli BL21(DE3) B strain lysogen, placUV5-T7 RNAPol (IPTG inducible) (Studier, 1990)

10 Plasmids

pSJ150 - Jorgensen et al. (1991)

pJW2 - Wang et al. (1990)

pET3a - Rosenberg et al. (1987)

pT7-7 - Obtained from Stan Tabor, Dept. of Biol. Chem., Harvard Medical School

15 pLysE and pLysS - pACYC184::T7 lysozyme from ptet and opposite orientation (Studier, 1990).

General Methods

Standard DNA manipulations were performed essentially as described in Sambrook et al. (1989).

20 Restriction enzymes, T4 DNA ligase, DNA Polymerase I (Klenow fragment) were obtained from Boehringer Mannheim or Promega and used as recommended by the supplier.

Chicken egg white lysozyme was obtained from Sigma.

Preparation of plasmids and transformation of E. coli was carried out as described
25 in Sambrook et al. (1989).

SDS-polyacrylamide gels were prepared, electrophoresed and stained as described in Sambrook et al. (1989).

Protein molecular weight markers were purchased from Sigma.

Lipase analysis

- 5 Lipase activity was detected on plates containing either glycerol tributyrate or an olive oil emulsion and brilliant green. Lipase activity was measured by a pH-stat method using glycerol tributyrate as substrate. 1 LU (lipase unit) is the amount of enzyme which liberates 1 umole titratable butyric acid per minute under the following conditions:

10	Temperature	30.0°C
	pH	7.0
	Emulsifier	Gum Arabic, 1 g/l
	Substrate	Glycerol tributyrate, 50 ml/l (Jørgensen et al., 1991)

- 15 A lipase screening assay was performed in microtiter dishes according to the following procedure:

First an emulsification reagent is made up:

17.9 g NaCl + 0.41 g KH_2PO_4 + 6.0 g Gum Arabic + 540 ml glycerol is brought to a final volume of 1000 ml with demineralized water.

- 20 The lipase assay reagent is made up as follows:

12.5 ml of the above emulsification reagent + 3.75 ml of glycerol tributyrate + 0.25 ml Brilliant green (40 mg/ml in H_2O) + 50 ml of 10 mM Tris pH 9.0 is emulsified for 1 min in an Ultra Turrax emulsifier.

The actual assay is performed by mixing 100 μ l of this assay reagent with 100 μ l of the lipase sample. The color development is compared to that of a known lipase sample.

The brilliant green plates consisted of 15 ml LB agar, with a top layer of 3 ml LB agar containing 0.3 ml of a 10% olive oil emulsion and 0.1 ml of a 40 mg/ml solution of brilliant green in distilled water. The olive oil emulsion was olive oil 10 ml + Gum Arabic 1 g + deionised water 90 ml, mixed using an Ultra Turrax emulsifier.

Induction of E. coli cultures for high level expression

(a) pJW2 based plasmids

- 10 Overnight cultures were grown at 30°C in an orbital shaker at 250 rpm, diluted 1:100 and grown for 3-4 hrs at 30°C until an A600 of 0.5 was reached. One of a set of duplicate cultures was then shifted to 42°C for induction of protein synthesis. Samples from both cultures were taken at time = 0, 30, 60, 90 and 120 minutes after induction.

15 (b) pET3a/pT7-7 based plasmids

- Overnight cultures were grown at 37°C in an orbital shaker at 250 rpm, diluted 1:50 and grown at 37°C until an A600 of 0.5 was reached. IPTG was then added to a final concentration of 1.5 mM to one of a set of duplicate cultures. Rifampicin may also be added to the induced culture 15 min after IPTG addition to a final concentration
20 of 100 μ g/ml. Samples from both cultures were taken at time = 0, 30, 60, 90 and 120 minutes after induction.

Treatment and preparation of protein samples

- Samples were immediately cooled to 0°C. Cells were harvested by centrifugation in a microfuge at 12,000 g for 5 min at 4°C. Cell pellets were resuspended in Laemmli
25 sample buffer and frozen at -20°C. Proteins were precipitated from the supernatants by addition of an equal volume of acetone and leaving on ice for 30 min followed by centrifugation for 15 min at 12,000 g at 4°C. The precipitated proteins were resuspended in Laemmli sample buffer and frozen at -20°C.

Analysis of proteins by SDS-polyacrylamide gel electrophoresis

Protein samples were boiled for 5 min prior to loading on 12% SDS-polyacrylamide gels. The gels were electrophoresed in Tris-glycine until the dye front reached the gel end and were then stained in 0.25% coomassie brilliant blue and destained in 5 10% acetic acid.

Western analysis

The method used was equivalent to that of Towbin et al. (1979). Protein samples were electrophoresed in 12% SDS-polyacrylamide gels and electrophoretically transferred to nitrocellulose. Filters were preincubated with blocking buffer and then incubated with anti-lipase antibody. Alkaline phosphatase-conjugated goat anti-rabbit 10 IgG (Sigma) was then incubated with the filter. NitroBlue Tetrazolium and 5-bromo-4-chloro-indolyl phosphate (both from Sigma) were used to visualize the proteins.

Method for Cell Lysis: adapted from Marston (1987)

15 Overnight cultures were diluted 1:100 into 100 mls LB medium and grown to an OD600 value of 0.5. Induction with heat in the case of pAHE2 and pAHE10 and IPTG in the case of pCBE6 was carried out for 2 hours. The cultures were then centrifuged at 500 g for 15 minutes at 4°C. The supernatant was removed and the pellet was weighed. For each gram (wet weight) of E. coli cells, 3 ml of lysis buffer was added 20 and the pellet was resuspended. Lysis Buffer contained 50 mM Tris.Cl, 1mM EDTA, 100 mM NaCl.

For each gram of cells, 8 ml of a 50 mM PMSF stock and 80 μ l of lysozyme (10mg/ml) was added and stirred for 20 minutes. 4 mg of deoxycholic acid was added per gram of cells while stirring continuously. The lysate was placed at 37°C and stirred 25 with a glass rod. When the lysate became viscous 20 μ l of DNAaseI (1mg/ml) was added per gram of cells. The lysate was placed at room temperature until it was no longer viscous (approx 30 minutes). The cell lysate was then stored at 4°C until required.

Purification and washing of inclusion bodies: (Marston et al 1984)

The cell lysate was centrifuged at 12000 g for 15 minutes at 4°C. The supernatant was decanted and the pellet was resuspended in 9 volumes of lysis buffer containing 0.5% Triton and 10mM EDTA(pH8.0). Storage at room temperature for 5 minutes was followed by centrifugation at 12000 g for 15 minutes at 4°C. The supernatant was decanted and set aside and the pellet was resuspended in 100 µl of H₂O. 10 µl samples were removed from the supernatant and the resuspended pellet and were mixed with 10 µl of 2X SDS gel loading buffer and analyzed by SDS-polyacrylamide gel electrophoresis to determine if most of the protein of interest is in the pellet. The lipase screening assay was also carried out to determine if most of the lipase activity of pAHE2 was in the pellet fraction.

Solubilization of inclusion bodies and renaturation: (adapted from Marston et al., (1984))

100 µl of lysis buffer containing 0.1 mM PMSF (added fresh), 8M Urea (deionized), and 0.1 M beta-mercaptoethanol was added to the washed pellet and stored for 1 hour at room temperature. The lipase activity screening assay was carried out in order to observe whether the lipase activity had disappeared due to the protein being totally denatured. 50 µl of each of the denatured protein samples were placed in dialysis tubing. The protein samples were dialysed in a buffer of 50 mM KH₂PO₄ (pH10.7), 1 mM EDTA (pH8.0), 50 mM NaCl and which also contained 8 M urea and 0.1 M BME. The pH was maintained at 10.7 with KOH. Initial dialysis in 8 M urea was carried out overnight. Further dialyses using a lower concentration of urea (ie 6 M; 4 M; 2 M; 0 M) were carried out in the above buffer in the absence of BME. The pH in these dialysis reactions was maintained at 8.0 using HCl. Dialysis in each of the different concentrations of urea was allowed to take place for 6 hours. As a control experiment duplicate samples were dialysed exactly as above except in the absence of urea and BME.

The renatured samples were removed from the dialysis tubing and lipase activity of the samples was examined on glycerol tributyrates and brilliant green plates. The lipase activity was also examined using the microtitre lipase screening assay.

Recovery of proteins from SDS-polyacrylamide gels

The procedure for recovering proteins from SDS-polyacrylamide gels was described by Hager and Burgess (1980). Protein samples were electrophoresed on an SDS-polyacrylamide gel. After electrophoresis, the gel was removed into a tray, 5 rinsed with water and stained for 10 minutes with ice-cold 250 mM KCl and 1 mM DTT. The gel was destained in cold water containing 1 mM DTT and the protein band of interest was cut out. (A portion of the gel was stained with coomassie blue to stain molecular weight standards to ensure the correct band was cut out). The gel band was crushed through a 1 ml syringe with G18 needle and 1 ml of elution buffer 10 containing 0.1% SDS, 50 mM Tris/HCl (pH7.9), 0.1 mM EDTA, 5 mM DTT, and 200 mM NaCl, was added. The protein was allowed to elute for at least 1 hour at 25°C with occasional agitation. The mixture was centrifuged briefly to pellet the crumbled gel. The protein was precipitated from the supernatant by adding 4 volumes of cold acetone and incubating at -70°C for 20 min. The precipitated protein was centrifuged 15 and the pellet was allowed to dry.

Generation of anti-LimA anti-sera in rabbits

In order to raise antibodies against LimA, three rabbits were injected with purified LimA protein according to a schedule similar to that described by Vaitukaitis, (1981). The LimA protein was purified from preparative SDS-polyacrylamide gels. On day 1, 20 Lim in 10 mM sodium phosphate, pH 7.2 was mixed with complete Freund's adjuvant and injected intradermally at 10 sites in the back of each rabbit. On day 21 a booster injection, mixed with incomplete Freund's adjuvant, was injected intramuscularly into the leg of each rabbit. An identical booster was injected in the same way on day 31 of the schedule. A test bleed revealed that anti-Lim antibodies had been generated.

Media**LB**

per litre : 10 g bacto-tryptone
 5 g bacto-yeast extract
5 10 g NaCl

Plates contained 2% agar.

EXAMPLES**EXAMPLE 1****Constructions for high level LipA expression****10 (a) lipA + limA : pAHE2 and pAHE8**

Plasmid pAHE2 (Fig. 1) was constructed by subcloning the 2.264 kb NsiI fragment encoding both lipA+limA from pSJ150 (Jorgensen et al.,1991) into NdeI-digested pJW2 (Wang et al., 1990). Ligations were transformed into E. coli TG1 at 30°C and plasmid DNA mini-preparations were used to identify plasmids with insert in the
15 correct orientation. pAHE2 is one of a few correct constructs obtained. In pAHE2 the initiation codon of the lipase gene is immediately downstream from the phage T7 ribosome binding site.

E57 is E. coli strain JA221 transformed with pAHE2. When E57 is induced for high level protein production, lipase protein can be identified on SDS-polyacrylamide gels
20 (and by western analysis) and lipase activity can be detected on brilliant green and glycerol tributyrates plates and by the microtitre assay and by pH-stat method.

Plasmid pAHE8 (Fig. 2) was constructed by subcloning the 2.264kb NdeI fragment encoding lipA + limA from pAHE2 into the expression vector pET3a digested with

NdeI. Ligations were transformed into E. coli strain TG1 and plasmid DNA was prepared from transformants to identify the correct plasmids.

E73 is E. coli strain BL21(DE3) pLysS transformed with pAHE8. When E73 is induced for high level protein production, lipase protein (approx. MW 34kD) can be seen on SDS-polyacrylamide gels and lipase activity is detected on brilliant green and glycerol tributyrates plates and by the microtitre assay.

(b) lipA without limA : pAHE10

Plasmid pAHE10 (Fig. 3) is a derivative of pAHE2 from which 2/3rds of the coding region of the limA gene was deleted. Plasmid pAHE10 was constructed by digesting 10 pAHE2 with the restriction enzymes ClaI and NotI, followed by treatment with Mung Bean Nuclease. DNA of the size 6.3 kb was excised as a band from an agarose gel stained with ethidium bromide. The DNA was purified using a Gene Clean kit, ligated and transformed into competent E. coli TG1. Plasmid DNA mini-preparations were used to identify the correct clones.

15 E68 is E. coli JA221 transformed with pAHE10. When E68 is induced for high level protein production, lipase protein, in comparable quantities to that from pAHE2, can be seen on SDS-polyacrylamide gels and by western analysis, but no lipase activity can be detected.

EXAMPLE 2

20 **Constructions for high level LimA expression: pCBE6, pCBE7, pCBE12, pCBE18 and pCBE19**

Plasmid pCBE6 (Fig. 4), from which limA alone is expressed, was constructed by subcloning the 1.17 kb ClaI-SphI fragment from pSJ150 as a blunt-ended fragment into the expression vector pET3a digested with NdeI and treated with Klenow to 25 generate blunt ends. E. coli strain E102 is strain BL21 (DE3)pLysS transformed with pCBE6.

Plasmid pCBE7 (Fig. 5) was constructed by subcloning the same 1.2 kb *Cl*I-*S*phI fragment into the expression vector pT7-7. E103 is BL21(DE3) pLysS transformed with pCBE7. Upon induction of E102 and E103, a protein of molecular weight approx. 32 kD was observed.

- 5 Plasmid pCBE12 (Fig. 6) was constructed by subcloning the *B*glII-*B*amHI fragment of pCBE7 into pACYC177. Lim expressed from pCBE12 in trans to lipase expressed from pSJ518 (described in Fig. 3 of WO 90/00908) and pAHE10 gives rise to lipase activity.

Plasmids pCBE18 and 19 (Fig. 7 and 8) were constructed by subcloning the
10 *B*glII-*B*amHI fragment of pCBE7 into the *B*clI site of pLysS. Lim expressed from pCBE18 and 19 in trans to lipase from pAHE10 gives rise to lipase activity.

EXAMPLE 3

Growth/induction experiments to obtain high level protein expression

Cultures were induced to produce high levels of both LipA and LimA as follows. E.
15 coli strains E57 (JA221/pAHE2) and E68 (JA221/pAHE10) were grown overnight at 30°C at 250 rpm. The cultures were diluted 1:100 and grown at 30°C at 250 rpm until the A600 was 0.5. The cultures were then shifted to grow at 42°C. E. coli strain E102 (BL21(DE3)pLysS/ pCBE6) was grown overnight at 37°C, diluted 1:100 and grown until A600 was 0.5. IPTG was then added to the culture to a final concentration of
20 1.5mM. Fifteen minutes later rifampicin was added to a final concentration of 100 µg/ml. The culture was incubated at 37°C and shaken at 250 rpm throughout the growth. Samples were taken from each culture at 60, 90 and 120 minutes after induction.

Samples were analysed by SDS-polyacrylamide gel electrophoresis and by western
25 analysis using anti-serum raised against lipase, see Fig. 9 and 10. Lipase protein was observed to be induced in strains containing either pAHE2 or pAHE10, in

equivalent amounts. The lipase for the majority about 95% is larger than the mature lipase isolated from Pseudomonas cepacia and the size is consistent with that expected for the complete prelipase. Samples were also assayed for lipase activity by the microtitre assay. Lipase activity was observed from cultures of E57 (pAHE2, 5 lipA + limA), but none was observed from cultures of E68 (pAHE10, lipA only) or E102 (pCBE6, limA).

The results demonstrate that lipase protein is made in equivalent amounts in the presence and in the absence of the limA gene, but no lipase activity is detected in the absence of limA. Active lipase is only produced when the limA gene is also 10 present.

EXAMPLE 4

Purification of Lip and Lim

Overnight cultures of JA221/pAHE2; JA221/pAHE10; BL21/pLysS/pCBE6 and BL21 were diluted 1:100 into 100 mls LB medium and grown to an OD600 value of 0.5. 15 Induction with heat in the case of pAHE2 and pAHE10 and IPTG in the case of pCBE6 was carried out for 2 hours. The cultures were then centrifuged at 500 g for 15 minutes at 4°C.

Cells were lysed by the method described. The Lim protein was found to be in the soluble fraction of the cell lysate. The lipase was found to reside in inclusion bodies. 20 Inclusion bodies were prepared by a method adapted from Marston et al. (1984). Pure lipase and Lim proteins were prepared after SDS-PAGE of inclusion bodies and soluble lysate fractions, respectively, by a method described by Hager and Burgess (1980). Samples were separated by 12% SDS-PAGE. After electrophoresis, the gel was soaked in transfer buffer (10 mM CAPS, 10% methanol, pH11) for 20 min. The 25 gel was electroblotted onto Problott which had been pretreated in 100% methanol (5-10 sec) and distilled water (2 x 1 min) and then soaked in transfer buffer. Electroblotting was carried out at 200 mA for 3 hours in transfer buffer at room

temperature. The blot was removed from the sandwich, rinsed in distilled water and then in methanol (5-10 sec). The blot was then stained in Amido Black (0.1% w/v) in 1% (v/v) acetic acid, 40% (v/v) methanol for 1 min. The blot was rinsed in frequent changes of distilled water, air dried and stored at -20°C between layers of filter paper. The bands corresponding to LimA and prelipase were excised and sequenced directly on an Applied Biosystems 477A protein sequencer.

The following sequences were obtained:

LimA (pCBE6): TARGGRAPL-RRVVYGVAVG (SEQ ID NO 6)
preLipA (pAHE2) : ARTMRSRVVAGAVA-AMSIA (SEQ ID NO 7)
10 preLipA (pAHE10): ARTMRSRVVAGAV--AM-IA (SEQ ID NO 8)

Except for the fact that the N-terminal methionine has been cleaved off, the sequences are as expected for LimA and for preLipA as deduced from the DNA sequence.

Gel-purified LimA protein was used to raise polyclonal antibodies as described in the methods section.

The purity of the proteins was checked by further SDS-PAGE analysis.

EXAMPLE 5

Denaturation and renaturation of pAHE2 and pAHE10 LipA

Denaturation/renaturation experiments were carried out with LipA from either pAHE2 or pAHE10 (present in inclusion bodies) together with LimA (pCBE6 and present in the cell lysate). 60 μ l of inclusion bodies was mixed with varying volumes of pCBE6 cell lysate (0 - 30 μ l) and solubilized together in 8 M urea. Renaturation was carried out by dialysis against decreasing concentrations of urea. Experiments were

carried out in the presence and absence of 5% glycerol. The lipase activity was measured using the pH stat.

The results of this experiment (shown below) indicate that increasing percentages of lipase activity may be recovered by denaturing/renaturing in the presence of 5 increasing quantities of LimA, and that the presence of glycerol does not affect the recovery of lipase activity.

Results for pAHE2 and pAHE10 LipA

Inclusion bodies undiluted; LimA from lysate

Initial lipase activity measured for pAHE2(pJW2::lipA/limA) = 7.5 LU (volume 60 μ l)

10 Initial lipase activity measured for pAHE10(pJW2::lipA) = 0 LU

Denaturation and renaturation

Sample	No of LU denatured	No of LU recovered (-Glycerol)	No of LU recovered (+Glycerol)
<hr/>			
5 pAHE2 + 0 μ l LimA	7.5	5.3	5.3
pAHE2 + 10 μ l LimA	7.5	9.3	8.3
pAHE2 + 20 μ l LimA	7.5	12.3	9.0
pAHE2 + 30 μ l LimA	7.5	13.2	13.5
10 pAHE2 + non-LimA lysate, 30 μ l	7.5	5.0	nd.
<hr/>			
pAHE10 + 0 μ l LimA	0.0	0.0	0.0
pAHE10 + 10 μ l LimA	0.0	6.5	10.5
15 pAHE10 + 20 μ l LimA	0.0	8.3	8.5
pAHE10 + 30 μ l LimA	0.0	16.0	11.0
pAHE10 + non-LimA lysate, 30 μ l	0.0	0.0	nd.
<hr/>			

20 EXAMPLE 6

Denaturation and renaturation of pAHE2 and pAHE10 LipA

For this set of experiments the inclusion body fractions were diluted 1:10. Samples of pAHE2 and pAHE10 (Lip) inclusion bodies and pCBE6 (Lim) cell lysate were analysed by SDS-polyacrylamide gel electrophoresis. The Biorad protein assay was used to quantify the amount of proteins used in the denaturation/renaturation experiments. 10 μ l of pAHE2 inclusion bodies was determined to contain 10 μ g of protein; 10 μ l of pAHE10 inclusion bodies to contain 8 μ g of protein; and 10 μ l of pCBE6 lysate to contain 25 μ g total protein.

The results of this experiment (shown below) indicate that increasing the quantity of LimA in denaturation/renaturation reactions results in initially increasing recoveries of lipase activity. Addition of further quantities of LimA to the reactions is inhibitory.

Results for pAHE2 and pAHE10 Lipases

5 Inclusion bodies diluted 1:10; LimA from lysate

Sample dialysed	No of lipase units recovered.
pAHE2 10 μ l	0.4
pAHE2 " +10 μ l LimA	5.6
pAHE2 " +15 μ l LimA	5.7
10 pAHE2 " +20 μ l LimA	4.5
pAHE2 " +30 μ l LimA	9.5
pAHE2 " +40 μ l LimA	3.2
<hr/>	
pAHE10 10 μ l	0.0
15 pAHE10 " +10 μ l LimA	2.5
pAHE10 " +15 μ l LimA	7.8
pAHE10 " +20 μ l LimA	7.3
pAHE10 " +30 μ l LimA	3.5
pAHE10 " +40 μ l LimA	0.5

20

EXAMPLE 7

Lipase and prelipase from Pseudomonas cepacia DSM 3959

P. cepacia DSM 3959 (the strain from which lipA and limA were cloned) was induced to produce lipase by growth in LB media supplemented with 80 g/l oleyl alcohol, and
 25 extracellular, periplasmic and intracellular fractions were isolated as described by Neu and Heppel (1965).

Immunoblots (Fig. 11) and lipase activity analysis showed that the extracellular fraction contained only active, mature lipase, whereas the intracellular fraction contained only inactive prelipase.

5 Fraction	lipase activity	protein %	
		prelipase	lipase
Intracellular	-	100	nd
Extracellular	+	nd	100

When LimA was provided as an extract of E. coli BL21 (DE3) pLysS pCBE6, mature, extracellular lipase from P. cepacia could be reactivated quantitatively after 10 denaturation/renaturation only in the presence of LimA. No lipase activity was observed when intracellular prelipase was used in a similar experiment with or without LimA, as is apparent from the following table:

Cell fraction of <u>P. cepacia</u>	LU prior to denaturation	LU after renaturation
15 Intracellular fraction (prelipase)		
20 μ l + 0 μ l LimA	0.0	0.0
20 μ l + 10 μ l LimA	0.0	0.0
20 μ l + 20 μ l LimA	0.0	0.0
20 μ l + 30 μ l LimA	0.0	0.0
20 20 μ l + 30 μ l non-LimA lysate	0.0	0.0
Extracellular fraction (mature lipase)		
20 μ l + 0 μ l LimA	1.5	0.0
20 μ l + 10 μ l LimA	1.5	0.4
20 μ l + 20 μ l LimA	1.5	0.8
25 20 μ l + 30 μ l LimA	1.5	1.3
20 μ l + 30 μ l non-LimA lysate	1.5	0.0

The activation of lipase but not prelipase from *P. cepacia* by LimA during renaturation experiments is consistent with the results using lipase proteins produced in *E. coli*. The *E. coli* lipase samples are composed of approximately 5% mature lipase and 95% prelipase. The amount of lipase activity observed before 5 denaturation (pAHE2 only) and after renaturation (pAHE2 and pAHE10) is equivalent to approximately 5% of that expected from the total amount of lipase protein seen on SDS-PAGE.

EXAMPLE 8

Constructions for expression of mature LipA protein

10 Plasmids from which the lipase LipA was expressed in a form lacking the signal peptide, i.e. as mature lipase, were constructed. These are pAHE19 (Fig. 12), which contains a modified version of the lipA gene encoding the mature lipase followed by the limA gene, and pAHE22 (Fig. 13), which encodes the mature lipase without limA. They were constructed as follows:

15 The following DNA fragment was synthesized (standard methods):

<MluI><HindIII>

5'-CGCGTAAGCTTCACATTGAAAGGGGAGGAGAATCATGGCC-
3'- ATTCGAAGTGTAACCTTCCCCTCCTCTTAGTACCGG-

<MluI>

20 GCTGGCTACGCGGCGA -3' (SEQ ID NO 9)
CGACCGATGCGCCGCTGCGC-5' (SEQ ID NO 10)

This DNA fragment basically contains the *Bacillus licheniformis* amyL ribosome binding site and start codon located in front of the sequence encoding the amino acids AAGYAA (SEQ ID NO 11) from the N-terminal of the mature LipA protein.

This DNA fragment was ligated into MluI digested pSJ420 (identical to pSJ416 described in WO 90/00908, and pSJ838 was isolated as a plasmid in which the HindIII site in the synthetic DNA fragment was located proximal to the amyL promoter on pSJ420.

5 pSJ838 carries the amyL promoter, amyL RBS, the amyL signal peptide fused to the first 6 codons of lipA, amyL RBS, mature lipA, and limA.

By in vivo recombination from pSJ838 (essentially as described in Jørgensen et al., 1990) plasmid pSJ897 was obtained, which contains the amyL promoter, amyL RBS, and mature lipA followed by limA. Immediately upstream from the amyL RBS on
10 pSJ897 is the recognition sequence for restriction enzyme NdeI.

pAHE19 was constructed by ligation of the 4.9 kb NdeI-EcoRI fragment of pJW2, the 0.46 kb NdeI-BamHI fragment of pSJ897, and the 2.07 kb BamHI-EcoRI fragment of pSJ150.

pAHE22 was constructed from pAHE19 by ClaI + NotI digestion and ligation
15 following exonuclease S1 treatment to make ends blunt.

Upon induction, lipase activity was observed from E. coli JA221 containing pAHE19, but not from E. coli JA221 containing pAHE22.

EXAMPLE 9

Denaturation and renaturation of mature LipA with and without LimA

20 Mature lipase was provided as the soluble fraction following induction, harvest, and lysis of cells as described in methods, and was used in a denaturation/renaturation experiment in the presence and absence of a LimA containing cell lysate, as described in methods.

The results of this experiment (table below) shows that mature LipA produced in *E. coli* only in the presence of LimA can be renatured to give active lipase enzyme.

pAHE19: mature LipA, LimA.

pAHE22: mature LipA.

	LU before denaturation	LU after renaturation
5		
pAHE19 (100 μ l)	0.5	0.5
pAHE19 (100 μ l) + LimA (10 μ l)	0.5	0.5
pAHE19 (100 μ l) + LimA (20 μ l)	0.5	0.75
10 pAHE19 (100 μ l) + LimA (30 μ l)	0.5	0.75
pAHE19 (100 μ l) + non-LimA lysate (30 μ l)	0.5	0.25
pAHE22 (100 μ l)	0.0	0.0
pAHE22 (100 μ l) + LimA (10 μ l)	0.0	0.5
15 pAHE22 (100 μ l) + LimA (20 μ l)	0.0	0.75
pAHE22 (100 μ l) + LimA (30 μ l)	0.0	0.75
pAHE22 (100 μ l) + non-LimA lysate (30 μ l)	0.0	0.0

EXAMPLE 10

20 Cloning and sequence of lipD and limD from *P. cepacia* DSM 3401

Another isolate of *P. cepacia*, DSM 3401 also called strain 75-10A, produce a lipase with similarity to LipA from DSM 3959.

Cloning and sequencing of the lipase encoding DNA from DSM 3401 (using standard methods as described in WO 90/00908) revealed two genes, hereafter
25 referred to as lipD and limD with a relatively high homology to lipA and limA.

Due to the extreme GC content of the DNA, the sequence was difficult to determine, and there still remains some undetermined basepairs - at 4 positions in the lipD gene, and at two positions in the limD gene.

The limD start codon is positioned three basepairs downstream from the lipD stop 5 codon, as is the case for lipA and limA.

The DNA sequence encoding lipD is given in SEQ ID NO 1, and the corresponding protein sequence in SEQ ID NO 3. The DNA sequence encoding limD is given in SEQ ID NO 2, and the corresponding protein sequence in SEQ ID NO 4.

From an alignment study of the amino acid sequences of LipA and LipD it appeared 10 that there are 22 differences in the mature part of the enzyme, in addition to 5 positions where the LipD aminoacid sequence could not be deduced.

From an alignment study of the amino acid sequences of LimA and LimD it appeared that there are 32 differences, in addition to 2 positions where the LimD amino acid sequence could not be deduced.

15 Based on these studies it is clear that LipD and LipA as well as LimD and LimA are homologous, but still different lipase and lipase modulator proteins.

It was therefore of interest to see if LimA could activate LipD in a denaturation/renaturation experiment.

EXAMPLE 11

20 Denaturation/renaturation experiments with LipD purified from P. cepacia

LipD from strain 7510-A (=DSM3401) was provided as a partially purified protein from DSM3401, using standard protein purification methods.

Denaturation/renaturation experiments were carried out using the lipase from strain 7510-A in the presence and absence of LimA. 18 LU were denatured and renatured with varying ratios of LimA and the recovered lipase activity was measured. Lipase activity was measured on the pH-stat. As control, the experiments were also carried out in the absence of urea.

The results obtained show that when the 7510-A lipase was denatured and renatured in the absence of LimA effectively no lipase activity was recovered. When increasing levels of LimA were added to the 7510-A lipase increasing levels of lipase activity were observed. However, the percentages of lipase activity recovered were still very low.

Results for 7510-A lipase

13,000 LU/ml stock used; LimA from lysate

Sample dialysed	No of LU denatured	No of LU recovered (+UREA)	% recovery
15 7510A 15 μ l	18	0.25	1.4
7510A " + 5 μ l LimA	18	0.25	1.4
7510A " +10 μ l LimA	18	0.4	2.2
7510A " +15 μ l LimA	18	0.35	2.0
20 7510A " +30 μ l LimA	18	0.45	2.5

An explanation for the low recovery of lipase activity was later found. It turned out that the lipase in this particular preparation was degraded during denaturation/renaturation, so the experiment was repeated with a new, partly purified preparation of lipase from DSM3401 and LimA from induced BL21(DE3) pLysS pCBE6. The following results show that LimA is well able to activate LipD.

	LU before denatura- tion	LU after renatura- tion	% re- covery
LipD (10 μ l) +	80	0.1	0.08
5 LipD (10 μ l) + 5 μ l LimA	80	44	35
LipD (10 μ l) + 10 μ l LimA	80	45	36
LipD (10 μ l) + 20 μ l LimA	80	56	45
LipD (10 μ l) + 30 μ l LimA	80	55	44
LipD (10 μ l) + 40 μ l LimA	80	53	42

10 EXAMPLE 12

Constructions for LipD expression

The lipA sequence contains a MluI site at a position corresponding to 7 amino acids into the mature LipA sequence and a ClaI site following the lipA stop codon.

The lipD sequence contains MluI and ClaI sites at the equivalent positions.

15 Therefore, plasmids could easily be constructed based on the former lipA expression vectors by insertion of the lipD MluI-ClaI fragment in stead of the lipA MluI-ClaI fragment to allow expression of a hybrid protein, in which only the first 7 amino acids in the mature protein are from LipA, whereas the rest of the mature protein is from LipD.

20 pAHE16 (Fig. 14) expresses the LipA-LipD hybrid lipase together with LimA, and was constructed from pAHE2 by replacement of the MluI-ClaI fragment as described above. pAHE23 (Fig. 15) expresses only the LipA-LipD hybrid lipase, and no Lim protein. It was constructed from pAHE16 by deletion of the ClaI-NotI fragment of LimA.

EXAMPLE 13**Denaturation/renaturation of the lipA-LipD hybrid lipase**

The LipA-LipD hybrid protein expressed from pAHE16 and pAHE23 was used in a denaturation/renaturation experiment with and without LimA added as described in 5 methods.

The lipase sample used in this experiment was the soluble fraction following lysis of the induced *E. coli* JA221 cells containing either pAHE16 or pAHE23 (although the vast majority of the lipase protein upon induction resides in inclusion bodies, the soluble fraction still contains some lipase, and there seem to be relatively more 10 mature lipase in the soluble fraction than in the inclusion bodies).

LimA was obtained from an induced culture of BL21(DE3) pLysS pCBE6.

The results presented below show that LimA is able to activate the LipA-LipD hybrid lipase in a denaturation/renaturation experiment.

	LU before denaturation	LU after renaturation
15		
pAHE16 (30 μ l) +	0.5	0.5
pAHE16 (30 μ l) + LimA (10 μ l)	0.5	0.75
pAHE16 (30 μ l) + LimA (20 μ l)	0.5	0.75
pAHE16 (30 μ l) + LimA (30 μ l)	0.5	0.75
20 pAHE16 (30 μ l) + LimA (40 μ l)	0.5	1.0
pAHE16 (30 μ l) + non-LimA cell lysate (40 μ l)	0.5	0.5
pAHE23 (30 μ l) +	0.0	0.0
pAHE23 (30 μ l) + LimA (10 μ l)	0.0	0.75
25 pAHE23 (30 μ l) + LimA (20 μ l)	0.0	0.75

37

pAHE23 (30 μ l) + LimA (30 μ l)	0.0	1.0
pAHE23 (30 μ l) + LimA (40 μ l)	0.0	1.0
pAHE23 (30 μ l) + non-LimA cell lysate (40 μ l)	0.0	0.0

5 EXAMPLE 14

Construction of lip-lim fusion

Plasmid pSJ721 is a deletion derivative of pSJ377 in which 15 bp have been deleted at the *Cl*I site, deleting the *lipA* stop codon, and the codons for the first three amino acids of *lim* (Jørgensen et al., 1991). pSJ721 thus encodes a *Lim* protein which is fused to the eight amino acids following the *Sph*I site at the C-terminal of *lipA*. The 838 bp *Sph*I-*Not*I fragment of pSJ721 (which includes the C-terminal of *lip* fused to most of *lim*) and the 915 bp *Mlu*I-*Sph*I fragment of pSJ150 (which includes most of the lipase coding sequence) were ligated with pAHE8 digested with *Mlu*I and *Not*I, such that a lip-lim fusion plasmid was generated. Transformants were screened for loss of the *Cl*I site which is normally present at the beginning of the *limA* gene and which is absent in pSJ721, and should be absent in lip-lim fusion plasmids. A number of plasmids were deemed to be correct from restriction enzyme analysis. Six of these were named pCBF1-6 (Fig. 16).

E. coli BL21(DE3) pLysS was transformed with each of the fusion plasmids and transformants were grown and induced with IPTG. Plating on tributyrine plates and analysis of activity in broth samples revealed that these plasmids gave rise to lipase activity upon induction. Protein samples from both cells and broth were analysed on SDS-polyacrylamide gels and by western analysis using anti-lipase anti-serum. Only a lipase protein identical in size to the unprocessed lipase produced by pAHE2 or pAHE8 was detected. No proteins of the higher molecular weight expected were observed, even in samples taken early in time course induction experiments. Perhaps the artificial lip-lim fusion is particularly susceptible to proteolytic cleavage at the junction of the proteins.

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In the Sequence Listing below

SEQ ID NO 1 is the nucleotide sequence of lipD;

SEQ ID NO 2 is the nucleotide sequence of limD;

SEQ ID NO 3 is the amino acid sequence of LipD. The sequence is that of the
5 prelipase, the first amino acid residue of the mature lipase is A (amino acid residue
45).

SEQ ID NO 4 is the amino acid sequence of limD;

SEQ ID NO 5 is the nucleotide sequence of the lip-lim fusion gene;

SEQ ID NO 6-8 are the peptide fragments discussed in Example 4; and

10 SEQ ID NO 9-11 are the nucleotide and amino acid sequences shown in Example

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: NOVO NORDISK A/S
- (B) STREET: Novo Alle
- (C) CITY: Bagsvaerd
- (E) COUNTRY: DENMARK
- (F) POSTAL CODE (ZIP): DK-2880
- (G) TELEPHONE: +45 44448888
- (H) TELEFAX: +45 4449 3256
- (I) TELEX: 37304

(ii) TITLE OF INVENTION: A process for the preparation of an active lipase

(iii) NUMBER OF SEQUENCES: 11

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EP0)

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: WO PCT/DK91/00402
- (B) FILING DATE: 20-DEC-1991

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Pseudomonas cepacia
- (B) STRAIN: DSM 3401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGGCCAGAT CGATGCGTTC CAGGGTGGTG GCAGGGGCAG TGGCATGCGC GATGAGCGTC	60
GCGCCGTTTC CGGGGGCGAC CGCGGTGATG ACGCTTGCGA CGACGCACGC GGCATGGCG	120
GCGACCGCGC CCGCCGACGA CTACGCGACG ACGCGTTATC CGATCATCCT CGTGACGGG	180
CTCACGGGTA CCGACAAGTA CGCGGGCGTG CTCGAGTACT GGTACGGCAT CCAGGAAGAC	240
CTGCAGCAGC ATGGCGCGAC CGTCTACGTC GCGAACCTGT CGGGCTTCCA GAGCGACGAC	300
GGGCCGAACG GCGCGGGCGA ACAGTTGCTC GCGTACGTGA AGACGGTGCT CGCGGCGACG	360
GGCGCGACCA AGGTCAATCT CGTCGGCCAC NCGCAGGGCG GGCTCACGTC GCGTTACGTT	420
GCGGCTGTTC CGCCCGATCT CGTCGCGTCG GTGACGACGA TCGGCACGCC GCATCGTGCN	480
NCCGAGTTTC CCGACTTCGT GCAGGGCGTG CTCGCATACG ATCCGACCGG GCTTTCGTCA	540
TCGGTGATCG CGGCGTTCGT CAATGTGTTT GGAATCCTGA CGAGCAGCAG CCACAACACG	600
AACCAGGACG CACTCGCGTC GCTGAAGACG CTGACGACCG CCCAGGCCGC CGCGTACAAC	660
CAGAACTATC CGAGCGCGGG CCTCGGTGCG CCGGGCAGTT GCCAGACCGG CNNNCCGACG	720
GAAACCGTGC GGTNCAACAC GCATCTGCTG TATTCGTGGG CCGGCACGGC GATCCAGCCG	780
ACGCTCTCCG TGTTCCGGTG CACGGGCGCG ACGGACACGA GCACCATTCG GCTCGTCGAT	840
CCGGCGAACG CGCTCGACCC GTCGACGCTT GCGCTGTTTC GCACGGGCAC GGTGATGATC	900
AACCGCGGCT CGGGCCCGAA CGACGGGCTC GTATCGAAGT GCAGCGCGCT GTACGGCCAG	960
GTGCTGAGCA CGAGCTACAA GTGGAACCAT ATCGACGAGA TCAACCAGTT GCTCGGCGTG	1020
CGCGGCGCGA ATGCGGAAGA TCCGTCGCG GTGATCCGCA CGCATGCGAA.CCGGCTGAAG	1080
CTGGCGGGCG TG	1092

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas cepacia*
(B) STRAIN: DSM 3401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGGCGGCAC GTGAAGGGCG CGCGCCGCTG GC CGGGCGCG CTGCAGTCTA CGGTGTCGTG	60
GGGCTGGCGG CGATCGCCGG CGTCGCGATG TGGAGCGGGG CGGGATGGCA TCGCGGTACG	120
GGTAGCCTCG GCGAAGCGCC CGATCGGGCG GCAGTGGGCG GCGTGGCTGC GGCACCGCCG	180
CAGGCGGCCG TGCCGGCGAG CGCGGGCCTG CCGTCGTCGC TGGCCGGCTC CAGCGCGCCG	240
CGCGTGCCGC TCGATCGGGG CGGCCATCTC GCGAAGGTGC GC CGGTGCG CGATTTCTTC	300
GACTACTGCC TGACCGCGCA GAGCGACCTC AGTGGGCGCG CGCTCGATGC ACTCGTCGTG	360
CGCGAGATTG CCGCGCAGCT CGACGGCACG GCGGCGCAGG CCGAGGCGCT CGACGTGTGG	420
CATCGCTATC GTGCGTATCT CGACGCGCTC GCGAACTGC GCGATGCCGG CGCGGTCGAC	480
AAGTCCGACC TGGGCGCGCT GCAGCTCGCG CTCGACCAGC GCGCATCGAT CGCGTATCGC	540
ACGCTCGGCG ACTGGAGCCA GCCGTTCTTC GCGCGGAGC AGTGGCGGCA GCGCTACGAT	600
CTCGCGGGC TGAAGATCGC GCAGGATCGC ACGCTGACCG ATGCGCAGAA GGCCGAACGG	660
CTCGCGGCGC TGCAGCAACA GATGCCGGCC GACGAACCG CGGCTCAGCA GCGGGTCGAC	720
CGGCAGCGGG CCGCGATCGA CCAGAGTCCG NAGTTGCAGA AGAGCGGGAC GACGCCCAGT	780
GCGATGCGCG CGCAACTGAC GCAGACGCTC GGGCCCGAGG CCGCCGCGCG CGTCGGCCAG	840
ATGCAGCAGG ACGACGCATC GTGGCAGAGN CGCTACGCGG ACTATGCGGC GCAGCGCGCG	900
CAGATCGAGT CGGCCGGCCT GTCGCCGAG GGC CGGACG CGCAGATCGC CGCACTGCGG	960
CAGCGCGTGT TCACGAAGCC CGGCGAAGCC GTGCGCGCGG CGTCGCTCGA TCGCGGGGCG	1020
GGCAGCGCGC AG	1032

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 364 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas cepacia*

(B) STRAIN: DSM 3401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met	Ala	Arg	Ser	Met	Arg	Ser	Arg	Val	Val	Ala	Gly	Ala	Val	Ala	Cys
1				5					10					15	
Ala	Met	Ser	Val	Ala	Pro	Phe	Ala	Gly	Ala	Thr	Ala	Val	Met	Thr	Leu
			20					25					30		
Ala	Thr	Thr	His	Ala	Ala	Met	Ala	Ala	Thr	Ala	Pro	Ala	Asp	Asp	Tyr
			35				40					45			
Ala	Thr	Thr	Arg	Tyr	Pro	Ile	Ile	Leu	Val	His	Gly	Leu	Thr	Gly	Thr
			50			55					60				
Asp	Lys	Tyr	Ala	Gly	Val	Leu	Glu	Tyr	Trp	Tyr	Gly	Ile	Gln	Glu	Asp
65					70					75					80
Leu	Gln	Gln	His	Gly	Ala	Thr	Val	Tyr	Val	Ala	Asn	Leu	Ser	Gly	Phe
				85					90					95	
Gln	Ser	Asp	Asp	Gly	Pro	Asn	Gly	Arg	Gly	Glu	Gln	Leu	Leu	Ala	Tyr
			100					105					110		
Val	Lys	Thr	Val	Leu	Ala	Ala	Thr	Gly	Ala	Thr	Lys	Val	Asn	Leu	Val
			115				120					125			
Gly	His	Xaa	Gln	Gly	Gly	Leu	Thr	Ser	Arg	Tyr	Val	Ala	Ala	Val	Ala
			130			135					140				
Pro	Asp	Leu	Val	Ala	Ser	Val	Thr	Thr	Ile	Gly	Thr	Pro	His	Arg	Xaa
145					150					155					160
Xaa	Glu	Phe	Ala	Asp	Phe	Val	Gln	Gly	Val	Leu	Ala	Tyr	Asp	Pro	Thr
				165					170					175	
Gly	Leu	Ser	Ser	Ser	Val	Ile	Ala	Ala	Phe	Val	Asn	Val	Phe	Gly	Ile
			180					185					190		
Leu	Thr	Ser	Ser	Ser	His	Asn	Thr	Asn	Gln	Asp	Ala	Leu	Ala	Ser	Leu
			195				200					205			
Lys	Thr	Leu	Thr	Thr	Ala	Gln	Ala	Ala	Ala	Tyr	Asn	Gln	Asn	Tyr	Pro
						210					220				

Ser Ala Gly Leu Gly Ala Pro Gly Ser Cys Gln Thr Gly Xaa Pro Thr
 225 230 235 240
 Glu Thr Val Arg Xaa Asn Thr His Leu Leu Tyr Ser Trp Ala Gly Thr
 245 250 255
 Ala Ile Gln Pro Thr Leu Ser Val Phe Gly Val Thr Gly Ala Thr Asp
 260 265 270
 Thr Ser Thr Ile Pro Leu Val Asp Pro Ala Asn Ala Leu Asp Pro Ser
 275 280 285
 Thr Leu Ala Leu Phe Gly Thr Gly Thr Val Met Ile Asn Arg Gly Ser
 290 295 300
 Gly Pro Asn Asp Gly Leu Val Ser Lys Cys Ser Ala Leu Tyr Gly Gln
 305 310 315 320
 Val Leu Ser Thr Ser Tyr Lys Trp Asn His Ile Asp Glu Ile Asn Gln
 325 330 335
 Leu Leu Gly Val Arg Gly Ala Asn Ala Glu Asp Pro Val Ala Val Ile
 340 345 350
 Arg Thr His Ala Asn Arg Leu Lys Leu Ala Gly Val
 355 360

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas cepacia*
- (B) STRAIN: DSM 3401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ala Ala Arg Glu Gly Arg Ala Pro Leu Ala Arg Arg Ala Ala Val
 1 5 10 15
 Tyr Gly Val Val Gly Leu Ala Ala Ile Ala Gly Val Ala Met Trp Ser
 20 25 30

Gly Ala Gly Trp His Arg Gly Thr Gly Ser Val Gly Glu Ala Pro Asp
 35 40 45
 Ala Ala Ala Val Gly Gly Val Ala Ala Ala Pro Pro Gln Ala Ala Val
 50 55 60
 Pro Ala Ser Ala Gly Leu Pro Ser Ser Leu Ala Gly Ser Ser Ala Pro
 65 70 75 80
 Arg Val Pro Leu Asp Ala Gly Gly His Leu Ala Lys Val Arg Ala Val
 85 90 95
 Arg Asp Phe Phe Asp Tyr Cys Leu Thr Ala Gln Ser Asp Leu Ser Ala
 100 105 110
 Ala Ala Leu Asp Ala Leu Val Val Arg Glu Ile Ala Ala Gln Leu Asp
 115 120 125
 Gly Thr Ala Ala Gln Ala Glu Ala Leu Asp Val Trp His Arg Tyr Arg
 130 135 140
 Ala Tyr Leu Asp Ala Leu Ala Lys Leu Arg Asp Ala Gly Ala Val Asp
 145 150 155 160
 Lys Ser Asp Leu Gly Ala Leu Gln Leu Ala Leu Asp Gln Arg Ala Ser
 165 170 175
 Ile Ala Tyr Arg Thr Leu Gly Asp Trp Ser Gln Pro Phe Phe Gly Ala
 180 185 190
 Glu Gln Trp Arg Gln Arg Tyr Asp Leu Ala Arg Leu Lys Ile Ala Gln
 195 200 205
 Asp Arg Thr Leu Thr Asp Ala Gln Lys Ala Glu Arg Leu Ala Ala Leu
 210 215 220
 Gln Gln Gln Met Pro Ala Asp Glu Arg Ala Ala Gln Gln Ala Val Asp
 225 230 235 240
 Arg Gln Arg Ala Ala Ile Asp Gln Ser Pro Xaa Leu Gln Lys Ser Gly
 245 250 255
 Thr Thr Pro Asp Ala Met Arg Ala Gln Leu Thr Gln Thr Leu Gly Pro
 260 265 270
 Glu Ala Ala Ala Arg Val Gly Gln Met Gln Gln Asp Asp Ala Ser Trp
 275 280 285
 Gln Xaa Arg Tyr Ala Asp Tyr Ala Ala Gln Arg Ala Gln Ile Glu Ser
 290 295 300
 Ala Gly Leu Ser Pro Gln Gly Arg Asp Ala Gln Ile Ala Ala Leu Arg
 305 310 315 320

Gln Arg Val Phe Thr Lys Pro Gly Glu Ala Val Arg Ala Ala Ser Leu
325 330 335

Asp Arg Gly Ala Gly Ser Ala Gln
340

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2118 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) **HYPOTHETICAL: NO**

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGGCCAGGA	CGATGCGTTC	CAGGGTGGTG	GCAGGGGCAG	TGGCATGCGC	GATGAGCATC	60
GCGCCGTTTC	CGGGGACGAC	CGCGGTGATG	ACGCTCGCGA	CGACGCACGC	GGCAATGGCG	120
GCCACCGCGC	CCGCCGCTGG	CTACGCGGCG	ACGCGTTACC	CGATCATCCT	CGTGACGGG	180
CTCTCGGGTA	CCGACAAGTA	CGCCGGCGTG	CTCGAGTATT	GGTACGGCAT	CCAGGAGGAC	240
CTGCAACAGA	ACGGTGCGAC	CGTCTACGTC	GCGAACCTGT	CGGGTTTCCA	GAGCGACGAC	300
GGCCCGAACG	GGCGCGGGCA	ACAGTTGCTC	GCTTACGTGA	AGACGGTGCT	CGCGGCGACG	360
GGGGCGACCA	AGGTCAATCT	CGTCGGTCAC	AGCCAGGGCG	GCCTCTCGTC	GCGCTATGTT	420
GCTGCCGTCG	CGCCCGATCT	CGTTGCGTCG	GTGACGACGA	TCGGCCCAGC	CGATCGCGGC	480
TCCGAATTCG	CCGACTTCGT	GCAGGACGTG	CTCGCGTACG	ATCCGACCGG	GCTTTCGTCA	540
TCGGTGATCG	CCGCGTTCTG	CAATGTGTTT	GGGATCCTGA	CGAGCAGCAG	CCACAACACC	600
AACCAGGATC	CGCTCGCCGC	ACTGCAGACG	CTGACCACCG	CACGGGCCGC	CACGTACAAC	660
CAGAACTATC	CGAGCGCGGG	CCTGGGTGCG	CCGGGCAGTT	GCCAGACCGG	TGCGCCGACC	720
GAAACCGTCG	GCGGCAACAC	GCACCTGCTG	TATTCGTGGG	CCGGCACGGC	GATCCAGCCG	780
ACGCTCTCCG	TGTTCGGCGT	CACGGGCGCG	ACGGACACGA	GCACCCTTCC	GCTCGTCGAT	840
CCGGCGAACG	TGCTCGACCT	GTCGACGCTC	GCGCTGTTTG	GCACCGGCAC	GGTGATGATC	900

AACCGCGGCT CCGGGCAGAA CGACGGGCTC GTGTCGAAGT GCAGTGCGCT GTACGGCAAG	960
GTGCTGAGCA CGAGCTACAA GTGGAACCAC CTCGACGAGA TCAACCAGCT GCTCGGCGTG	1020
CGCGGCGCGT ATGCGGAAGA TCCCGTCGCG GTGATCCGCA CGCATGCGAA CCGGCTGAAG	1080
CTGGCGGGGG CACGAGGAGG ACGCGCGCCG CTGGCGCGCC GCGCCGTGGT CTATGGTGCC	1140
GTGGGGCTGG CGGCGATTGC CGGCGTGGCG ATGTGGAGCG GCGCGGGCCG GCATGGCGGG	1200
ACGGGCGCAT CCGGCGAGCC GCCGGATGCG TCGGCGGCAC GCGGACCGCG TGCCGCACCG	1260
CCGCAGGCCG CCGTGCCGGC AAGCACGAGC CTGCCGCCGT CGCTCGCCGG CTCCAGCGCG	1320
CCCCGCTTGC CGCTCGATGC CGGCGGCCAT CTCGCGAAGG CGCGCGCGGT GCGGGATTTC	1380
TTCGACTACT GCCTGACCGC GCAGAGCGAC CTGAGTGCGG CCGGGCTCGA TGC GTTCGTC	1440
ATGCGCGAGA TTGCCGACACA GCTCGACGGG ACCGTTGCGC AGGCCGAGGC GCTCGACGTG	1500
TGGCACCGET ATCGCGCGTA TCTCGACGCA CTCGCGAAAT TCGCGATGC CGGCGCGGTG	1560
GACAAGTCGG ACCTGGGTGC ATTGCAGCTC GCGCTCGACC AGCGCGCGTC GATCGCGTAC	1620
CGGTGGCTCG GCGACTGGAG CCAGCCGTTT TTCGGTGC GG AGCAATGGCG GCAGCGCTAC	1680
GACCTCGCGC GGCTGAAGAT CGCGCAGGAC CCCGCGCTGA CGGATGCGCA GAAGGCCGAA	1740
CGGCTCGCGG CGCTCGAACA GCAGATGCCG GCCGACGAAC GCGCCGCGCA GCAGCGCGTC	1800
GACCGGCAGC GCGCGGCGAT CGACCAGATC GCGCAATTGC AGAAGAAGCG GCGACGCC	1860
GATGCGATGC GCGCACAAC GACGCGAGCG CTCGGCCCCG AAGCGGCCGC GCGCGTCGCG	1920
CAGATGCAGC AGGACGACGC ATCGTGGCAG AGGCGCTACG CGGACTACGC GCGCGAGCGT	1980
GCGCAGATCG AGTCGGCCGG CCTGTCGCCG CAGGATCGCG ACGCGCAGAT CGCCGCGCTG	2040
CGGCGAGCGG TGTTTACGAA GCCCGGCGAA GCCGTGCGCG CGGCATCGCT CGATCGCGGG	2100
GCGGGCAGCG CGCGGTAA	2118

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas cepacia*

(B) STRAIN: DSM3959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Thr Ala Arg Gly Gly Arg Ala Pro Leu Arg Arg Ala Val Val Tyr Gly
1 5 10 15

Ala Val Gly

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas cepacia*

(B) STRAIN: DSM3959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Ala Arg Thr Met Arg Ser Arg Val Val Ala Gly Ala Val Ala Ala Met
1 5 10 15

Ser Ile Ala

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Pseudomonas cepacia
 - (B) STRAIN: DSM3959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ala Arg Thr Met Arg Ser Arg Val Val Ala Gly Ala Val Ala Met Ile
1 5 10 15
Ala

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CGCGTAAGCT TCACATTGAA AGGGGAGGAG AATCATGGCC GCTGGCTACG CGGCGA

56

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CGCGTCGCCG CGTAGCCAGC GGCCATGATT CTCCTCCCCT TTCAATGTGA AGCTTA

56

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas cepacia*

(B) STRAIN: DSM3959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Ala Ala Gly Tyr Ala Ala
1 5

CLAIMS

1. A process for preparing an active lipase enzyme in vitro, the process comprising
 - (a) culturing a host cell transformed with a DNA sequence encoding a lipase enzyme under suitable conditions to produce the lipase enzyme in inactive or partly active
5 form, recovering the lipase enzyme from the culture, and subjecting the recovered lipase enzyme to denaturation,
 - (b) mixing the denatured lipase enzyme obtained in step (a) with a chaperone molecule, and
 - (c) subjecting the mixture of step (b) to renaturation to produce the active lipase
10 enzyme.
2. A process for preparing an active lipase enzyme in vitro, the process comprising
 - (a) culturing a host cell transformed with a DNA sequence encoding a lipase enzyme under suitable conditions to produce the lipase enzyme in inactive or partly active
form and recovering the lipase enzyme from the culture,
 - 15 (b) mixing the recovered lipase enzyme with a chaperone molecule, and
 - (c) subjecting the mixture of step (b) to denaturation followed by renaturation to produce the active lipase enzyme.
3. A process according to claim 1 or 2, in which the chaperone molecule is produced by culturing a host cell transformed with a DNA sequence encoding the
20 chaperone molecule under suitable conditions to produce the chaperone molecule and recovering the chaperone molecule from the culture.

4. A process according to any of claims 1 - 3, in which the chaperone molecule is subjected to a denaturation treatment before being added to the denaturated lipase in step (b).
5. A process for preparing an active lipase enzyme in vitro, the process comprising
- 5 (a) culturing a host cell transformed with a DNA sequence encoding a lipase enzyme and with a DNA sequence encoding a chaperone molecule under suitable conditions to produce the lipase enzyme in inactive or partly active form and recovering a lipase enzyme chaperone molecule mixture from the culture, and
- (b) subjecting the mixture of step (a) to denaturation followed by renaturation to
10 produce the active lipase enzyme, optionally with addition of a further amount of chaperone molecule to the mixture.
6. A process according to any of claims 1 - 5, wherein the lipase enzyme is one derived from a Pseudomonas sp. or a Chromobacter sp.
7. A process according to claim 6, wherein the lipase enzyme is a Pseudomonas
15 cepacia, Pseudomonas fragi, Pseudomonas gladioli, Pseudomonas fluorescens, Pseudomonas stutzeri, Pseudomonas alcaligenes, Pseudomonas pseudoalcaligenes, Pseudomonas putida, Pseudomonas glumae, Pseudomonas aeruginosa or Chromobacter viscosum lipase, or a derivative of said lipase enzyme.
8. A process according to any of claims 1 - 7, wherein the host cell for the
20 production of the lipase enzyme is Escherichia coli.
9. A process according to claim 8, wherein the DNA sequence encoding the lipase enzyme is preceded by the promoter of the Bacillus stearothermophilus maltogenic amylase gene, Bacillus licheniformis α -amylase gene, Bacillus amyloliquefaciens α -amylase gene, Bacillus subtilis alkaline protease gene, or Bacillus pumilus xylosidase

gene, or by the phage Lambda P_R or P_L promoters, the phage T7 gene 10 promoter or the E. coli *lac* promoter.

10. A process according to claim 8, wherein the DNA sequence encoding the lipase enzyme is preceded by a ribosome binding site of of the Bacillus stearothermophilus maltogenic amylase gene, Bacillus licheniformis α -amylase gene, Bacillus amyloliquefaciens α -amylase gene, Bacillus subtilis alkaline protease gene, Bacillus pumilus xylosidase gene, phage T7 gene 10 or E. coli *lac* gene.

11. A process according to any of claims 1 - 10, wherein the lipase enzyme is produced intracellularly in a high yield.

10 12. A process according to claim 11, wherein the lipase enzyme is produced in the form of inclusion bodies.

13. A process according to any of claims 1 - 5, wherein the chaperone molecule is a Pseudomonas lipase modulator or a derivative thereof.

14. A process according to claim 13, in wherein the chaperone molecule is selected
15 from the group consisting of Pseudomonas cepacia lipase modulator, the Pseudomonas glumae lipase modulator, the Pseudomonas aeruginosa lipase modulator or a derivative thereof.

15. A process according to claim 3, wherein the host cell for the production of the chaperone molecule is E. coli.

20 16. A process according to claim 15, wherein the DNA sequence encoding the chaperone molecule is preceded by the promoter of the Bacillus stearothermophilus maltogenic amylase gene, Bacillus licheniformis α -amylase gene, Bacillus amyloliquefaciens α -amylase gene, Bacillus subtilis alkaline protease gene, or Bacillus pumilus xylosidase gene, or by the phage Lambda P_R or P_L promoters, the
25 phage T7 gene 10 promoter or the E. coli *lac* promoter.

17. A process according to claim 15, wherein the DNA sequence encoding the chaperone molecule is preceded by a ribosome binding site of of the Bacillus stearothermophilus maltogenic amylase gene, Bacillus licheniformis α -amylase gene, Bacillus amyloliquefaciens α -amylase gene, Bacillus subtilis alkaline protease gene,
5 Bacillus pumilus xylosidase gene, phage T7 gene 10 or E. coli *lac* gene.

18. A process according to any of claims 13 - 17, wherein the chaperone molecule is produced intracellularly in a high yield.

19. A process according to any of claims 1 - 18, wherein the lipase enzyme is a Pseudomonas cepacia lipase, and wherein the chaperone molecule is a
10 Pseudomonas cepacia lipase modulator.

20. A DNA construct comprising a first DNA sequence encoding a lipase enzyme fused to a second DNA sequence encoding a chaperone molecule in such a way that the lipase enzyme and chaperone molecule or functional part thereof are expressed as a single fusion protein on culturing a suitable host cell transformed
15 with the DNA construct.

21. A DNA construct according to claim 20, wherein the first DNA sequence encoding the lipase enzyme is one derived from a Pseudomonas sp. or a Chromobacter sp.

22. A DNA construct according to claim 21, wherein the first DNA sequence is one
20 encoding a Pseudomonas cepacia, Pseudomonas fragi, Pseudomonas gladioli, Pseudomonas fluorescens, Pseudomonas stutzeri, Pseudomonas alcaligenes, Pseudomonas pseudoalcaligenes, Pseudomonas putida, Pseudomonas glumae, Pseudomonas aeruginosa or Chromobacter viscosum lipase, or a derivative of said lipase enzyme.

25 23. A DNA construct according to claim 20, wherein the second DNA sequence is one encoding a Pseudomonas lipase modulator or a derivative thereof.

24. A DNA construct according to claim 23, wherein the second DNA sequence is one encoding a Pseudomonas cepacia lipase modulator, a Pseudomonas glumae lipase modulator, a Pseudomonas aeruginosa lipase modulator or a derivative thereof.
- 5 25. A DNA construct according to any of claims 20 - 24, wherein the first DNA sequence encodes a Pseudomonas cepacia lipase or a derivative thereof, and wherein the second DNA sequence encodes a Pseudomonas cepacia lipase modulator or a derivative thereof.
26. A DNA construct according to claim 25 which has the sequence shown in SEQ
10 ID No. 7 appended hereto.
27. A recombinant expression vector comprising a DNA construct according to any of claims 20-26.
28. A host cell transformed with a DNA construct according to any of claims 20-26 or with a recombinant expression vector according to claim 27.
- 15 29. A host cell according to claim 28 which is a cell of a strain of E. coli.
30. A host cell according to claim 29, wherein the DNA construct is preceded by the promoter of the Bacillus stearothermophilus maltogenic amylase gene, Bacillus licheniformis α -amylase gene, Bacillus amyloliquefaciens α -amylase gene, Bacillus subtilis alkaline protease gene, or Bacillus pumilus xylosidase gene, or by the phage
20 Lambda P_R or P_L promoters, the phage T7 gene 10 promoter or the E. coli *lac* promoter.

31. A host cell according to claim 29, wherein the DNA construct is preceded by the ribosome binding site of of the Bacillus stearothermophilus maltogenic amylase gene, Bacillus licheniformis α -amylase gene, Bacillus amyloliquefaciens α -amylase gene, Bacillus subtilis alkaline protease gene, Bacillus pumilus xylosidase gene, 5 phage T7 gene 10 or E. coli lac gene.

32. A process for preparing a lipase in active form, the process comprising culturing a host cell according to any of claims 28 - 31 under suitable conditions to produce the lipase, and recovering the lipase from the culture.

33. A process for denaturing and renaturing a lipase enzyme, the process 10 comprising

(a) subjecting a lipase enzyme to a denaturation treatment,

(b) mixing the denaturated lipase enzyme obtained in step (a) with a chaperone molecule, which optionally has been denaturated, and

(c) subjecting the mixture of step (b) to renaturation to produce the active lipase 15 enzyme.

34. A process for denaturing and renaturing a lipase enzyme, the process comprising

a) mixing a lipase enzyme to be subjected to a denaturation and renaturation treatment with a chaperone molecule, and

20 b) subjecting the mixture of step a) to denaturation followed by renaturation so as to produce an active lipase enzyme.

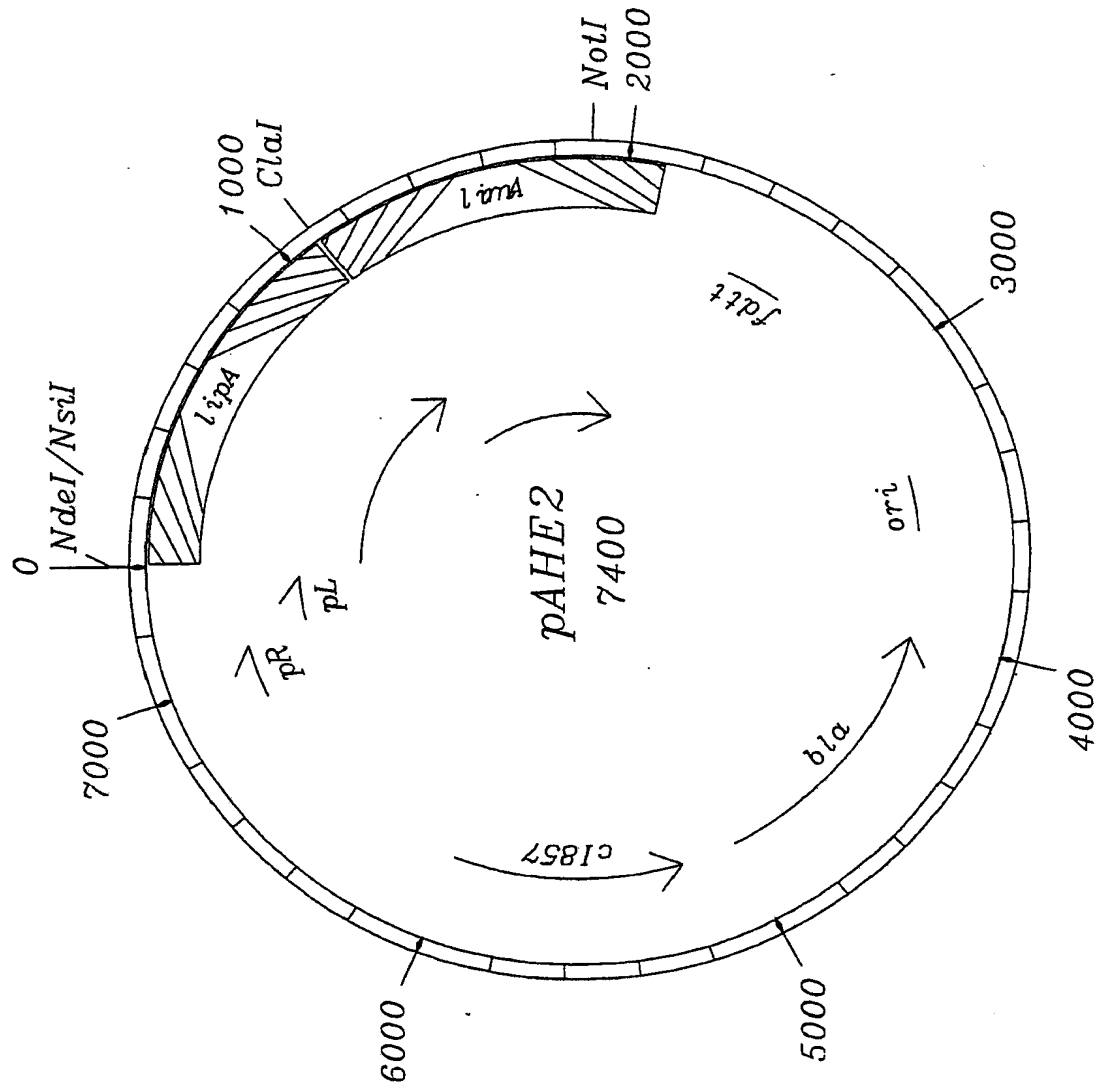


Fig. 1

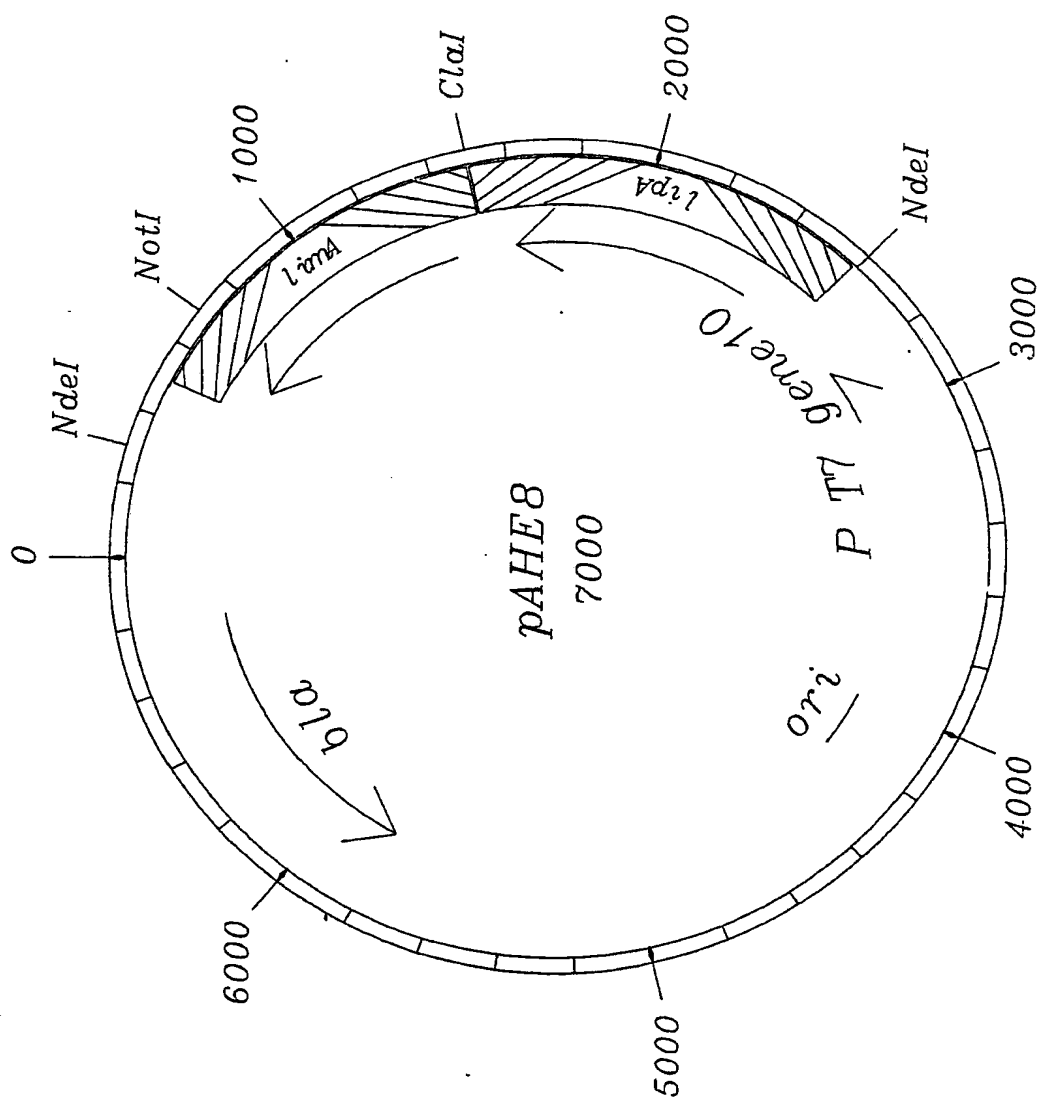


Fig. 2

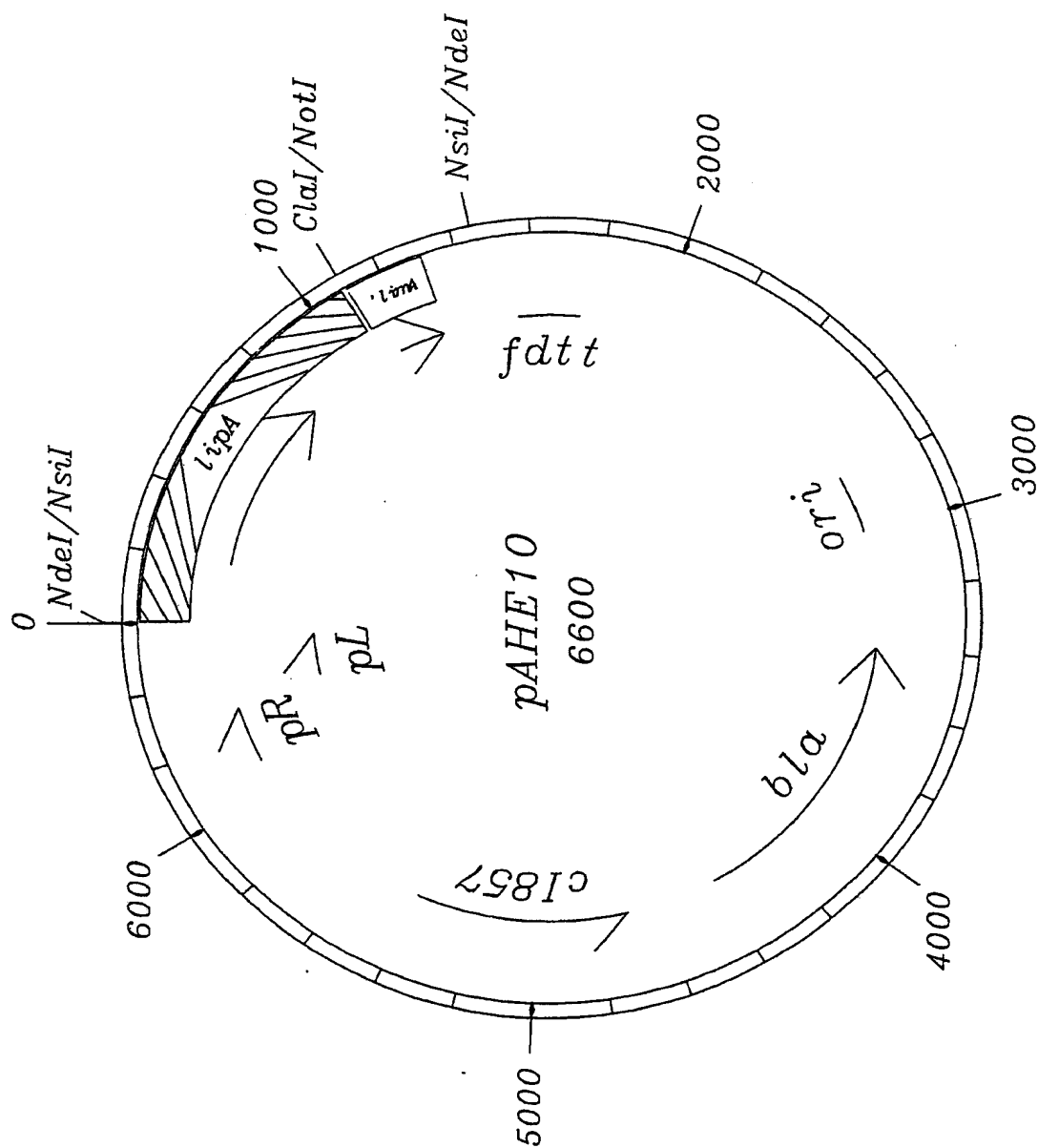


Fig. 3

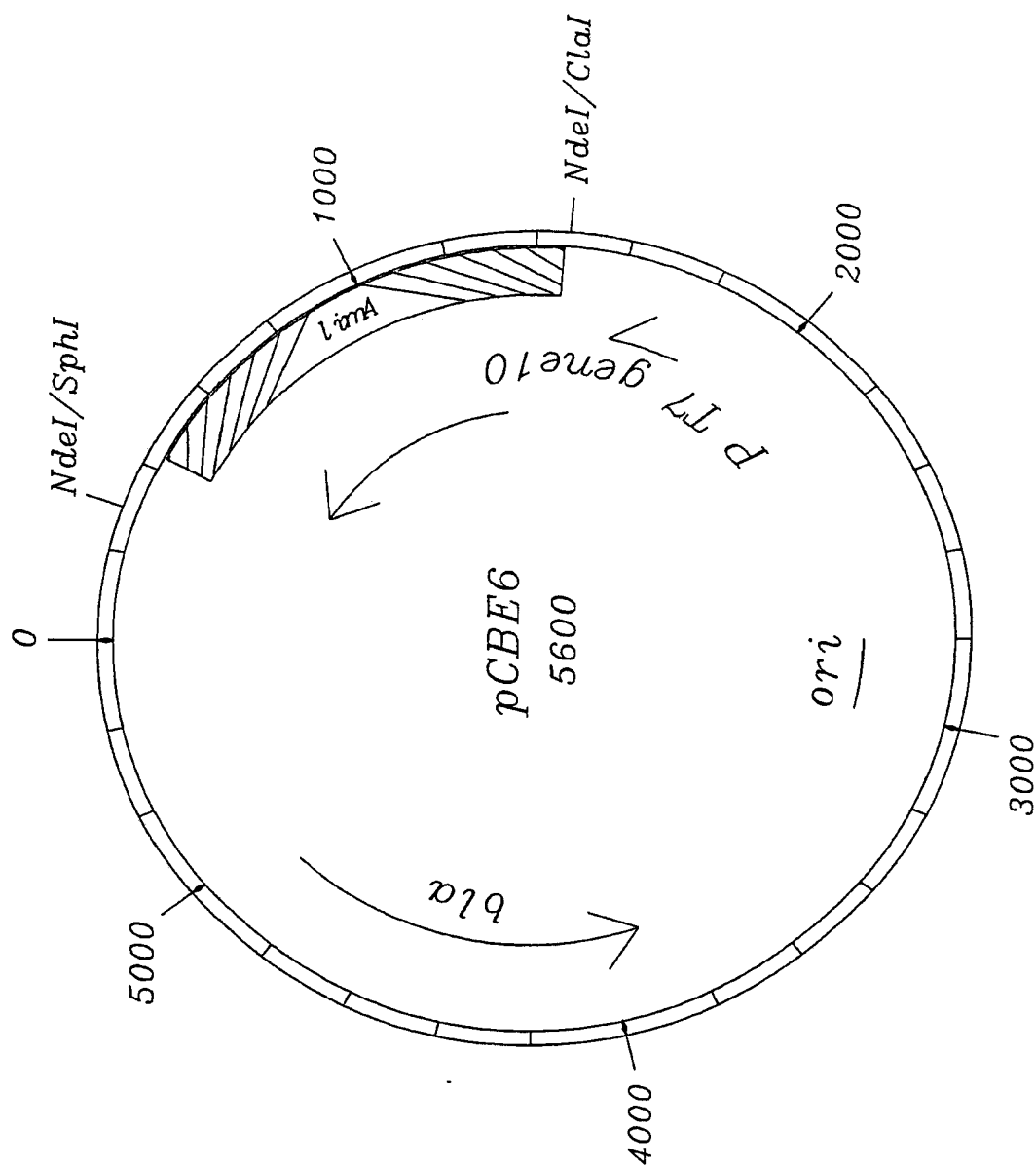


Fig. 4

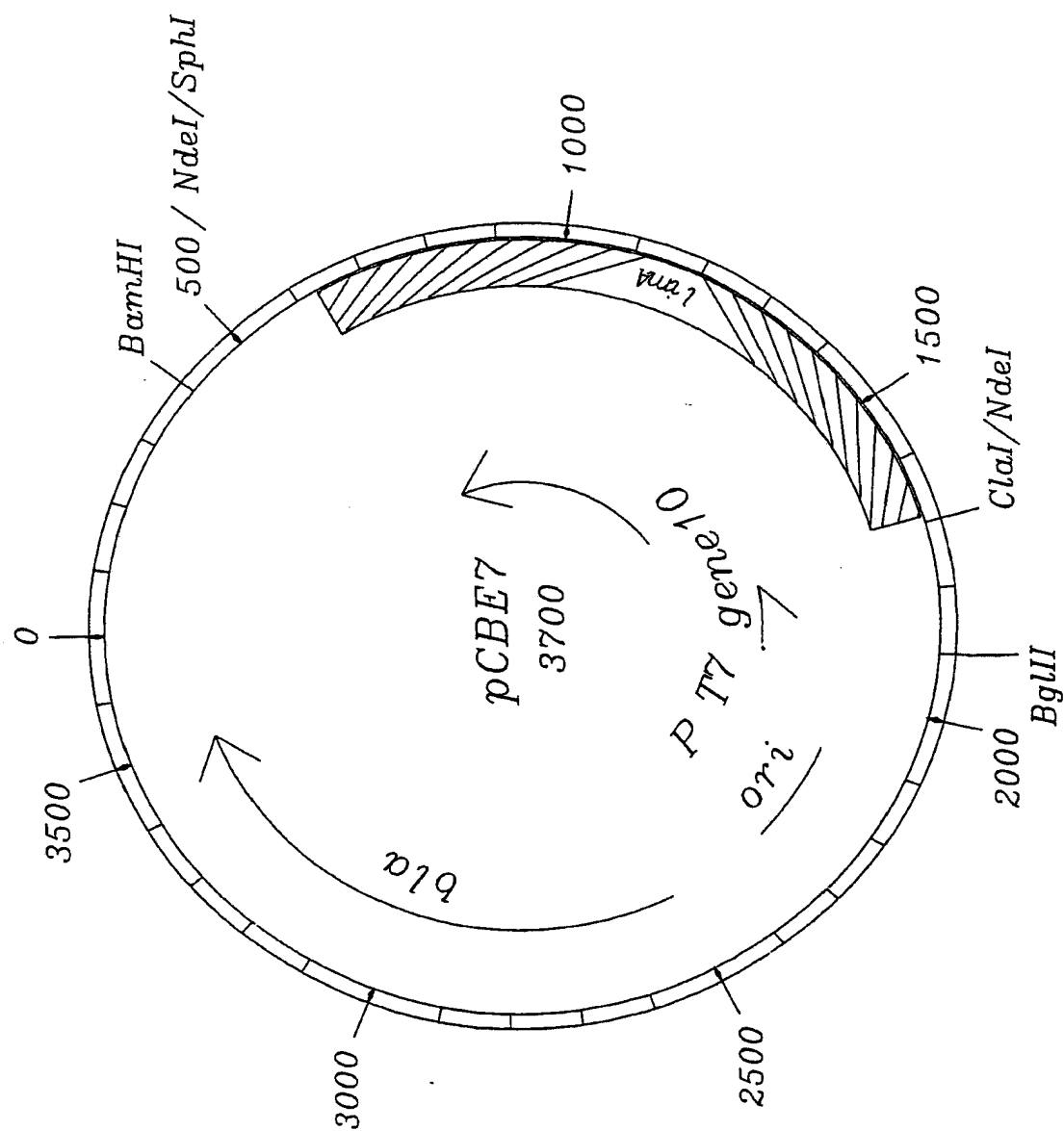


Fig. 5

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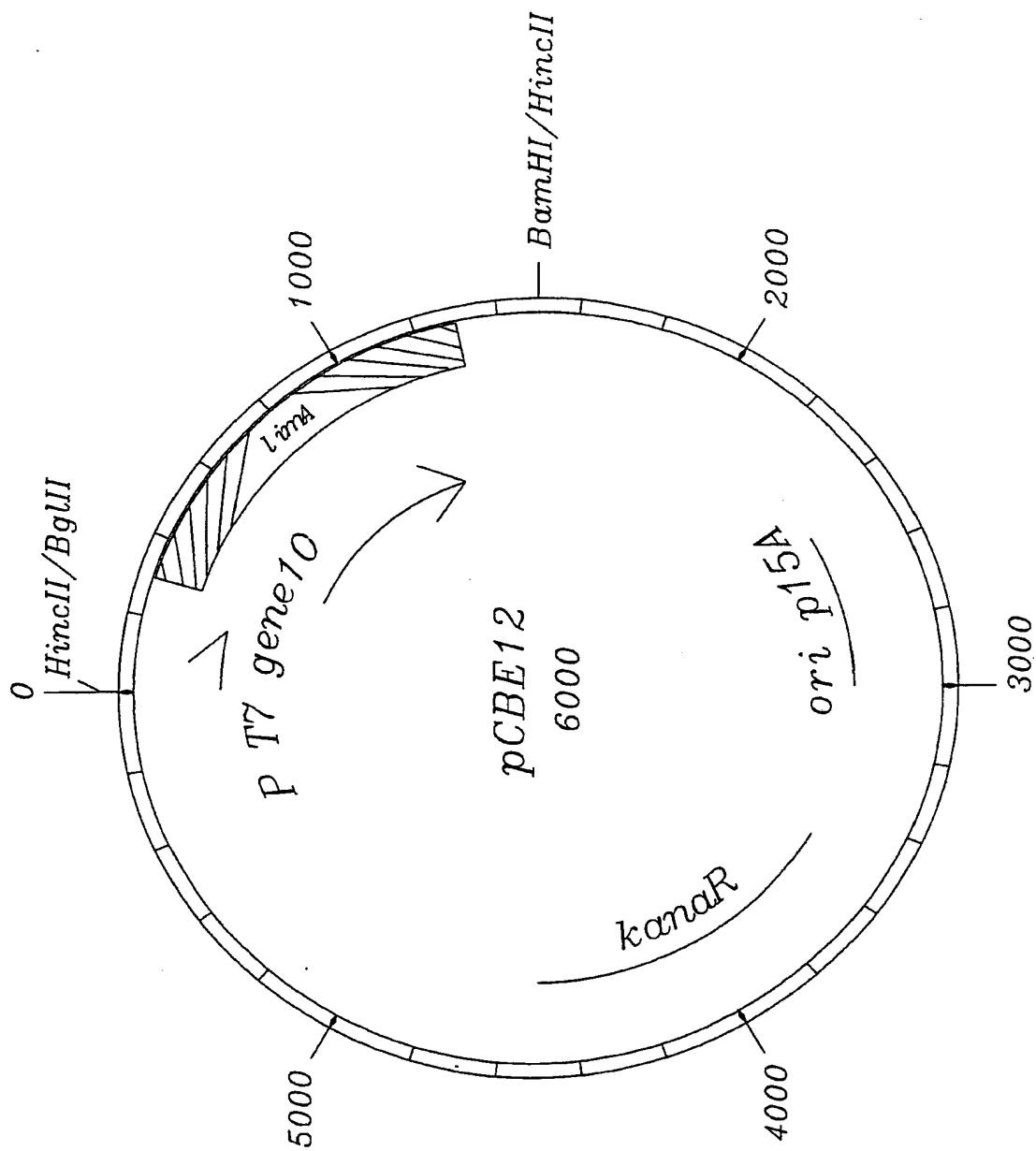


Fig. 6

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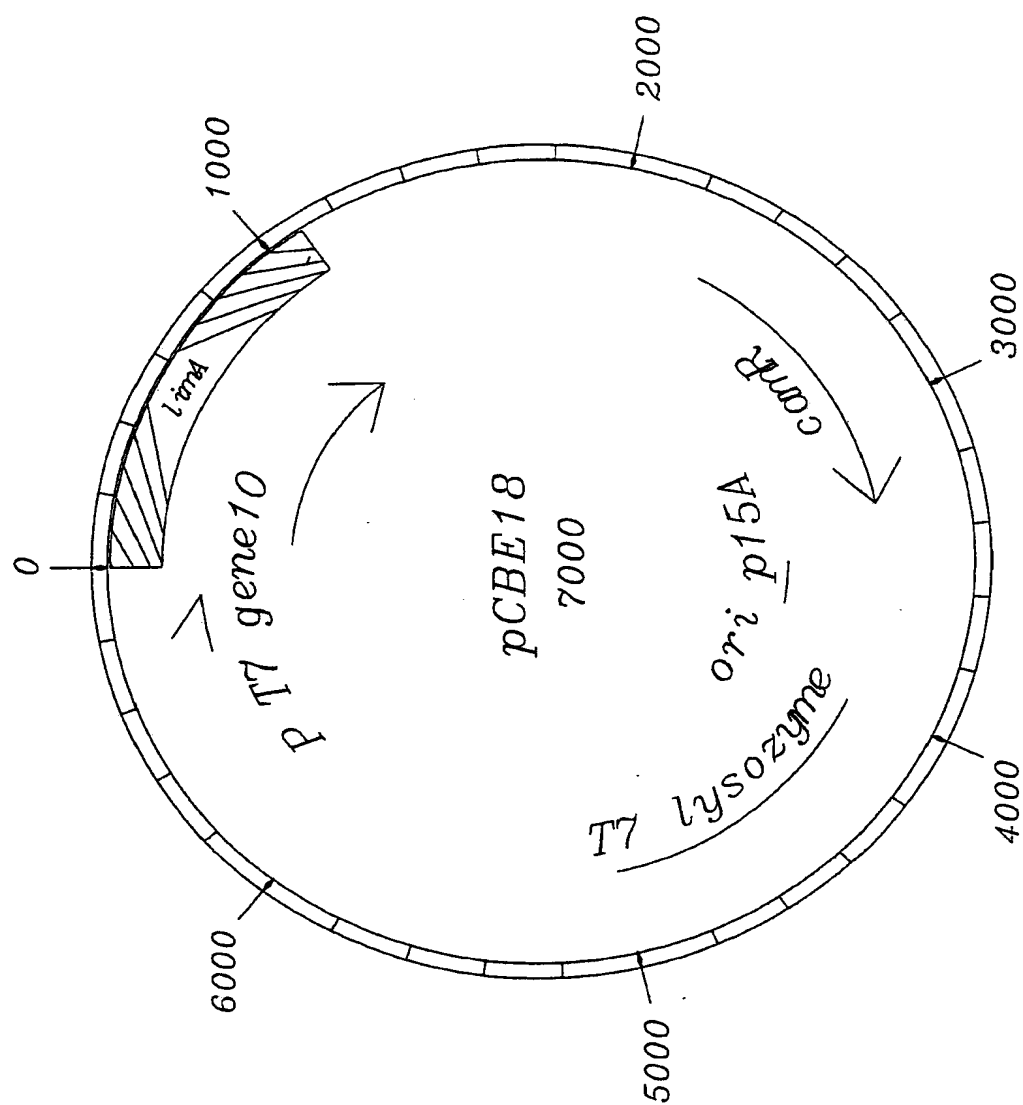


Fig. 7

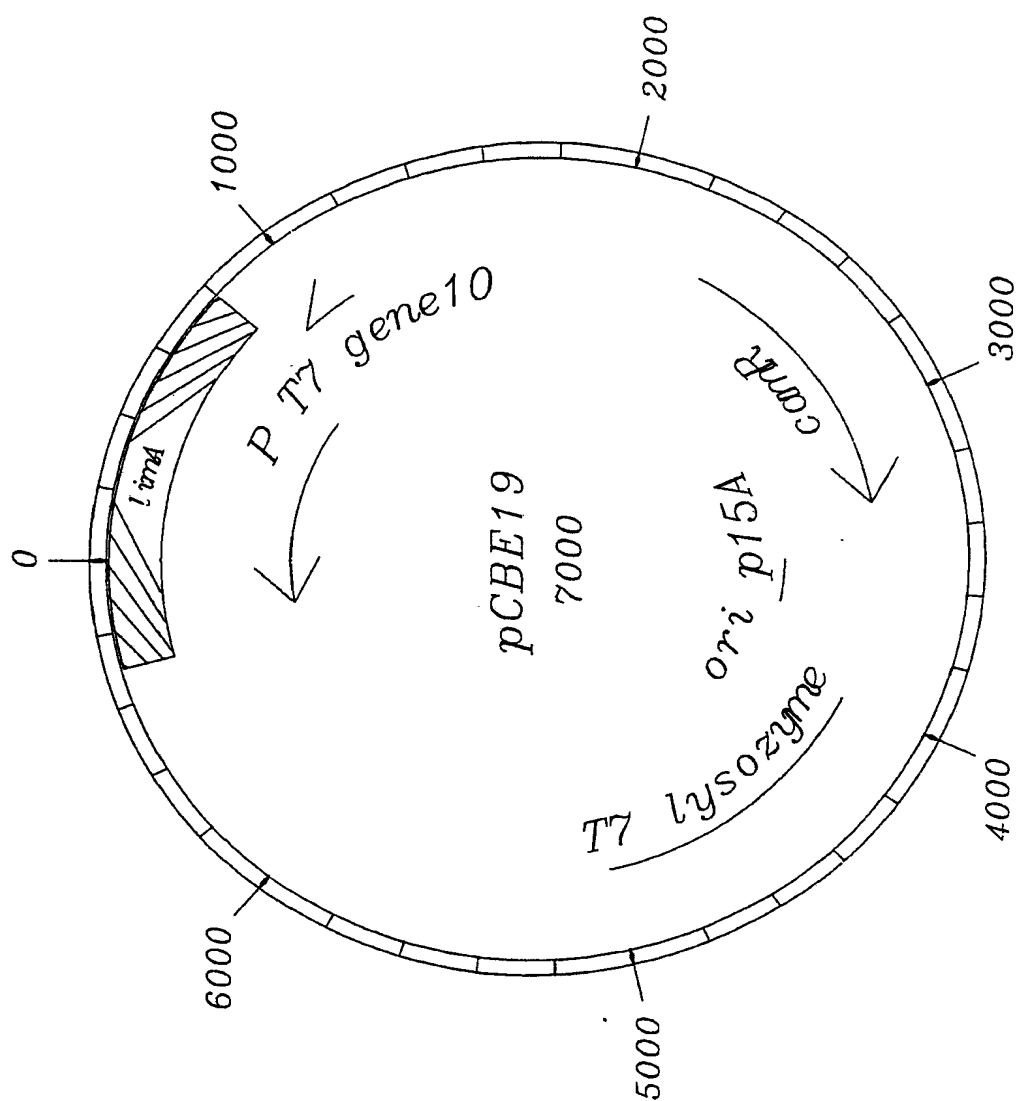


Fig. 8

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A B C D E F G H I J K L M N O P Q R S

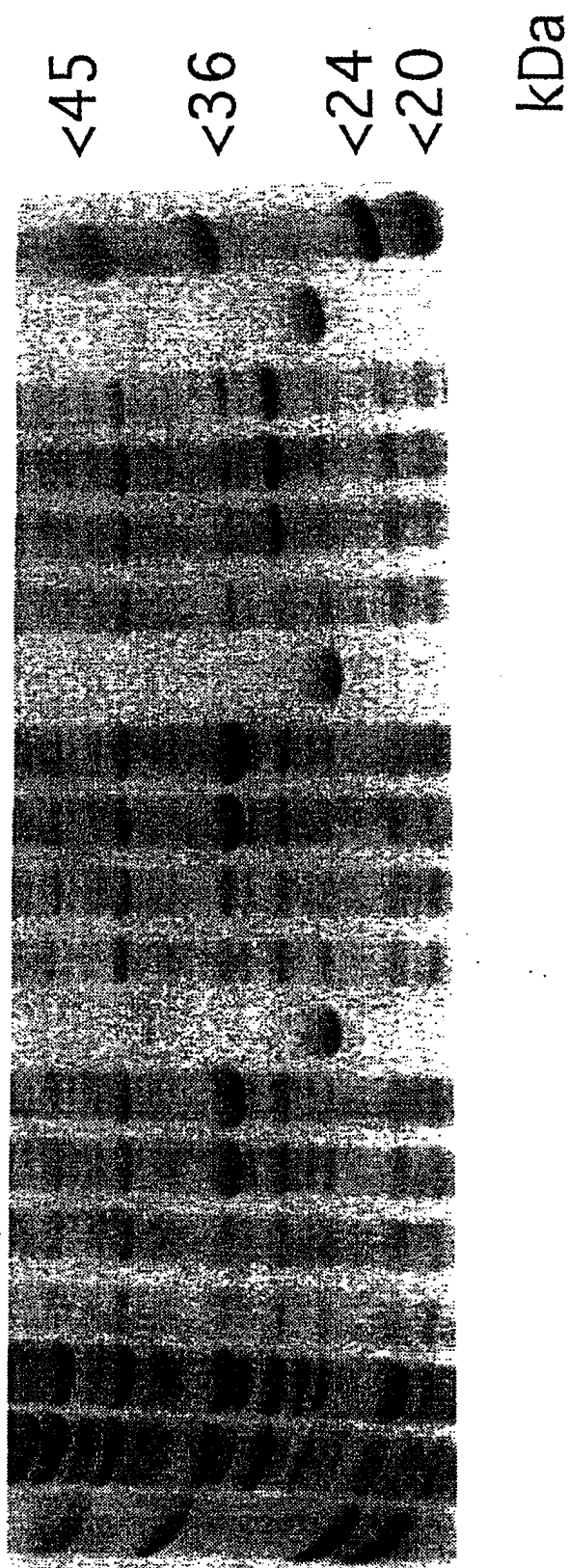


Fig. 9

A B C D E F G H I J K L M N O P Q R S Lipase

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< pre

< mature

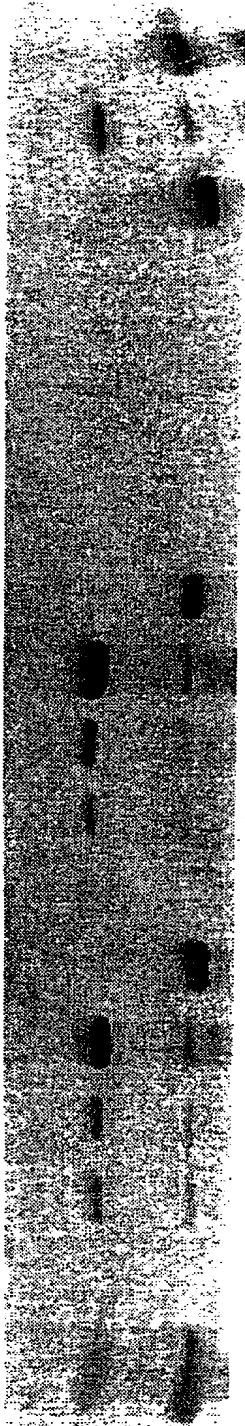


Fig. 10

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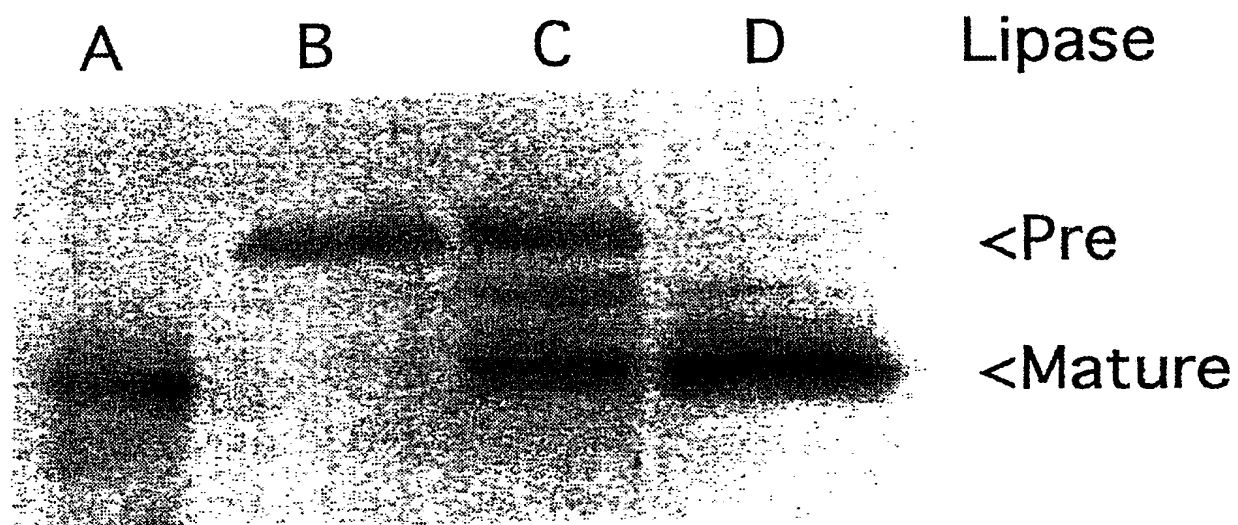


Fig. 11

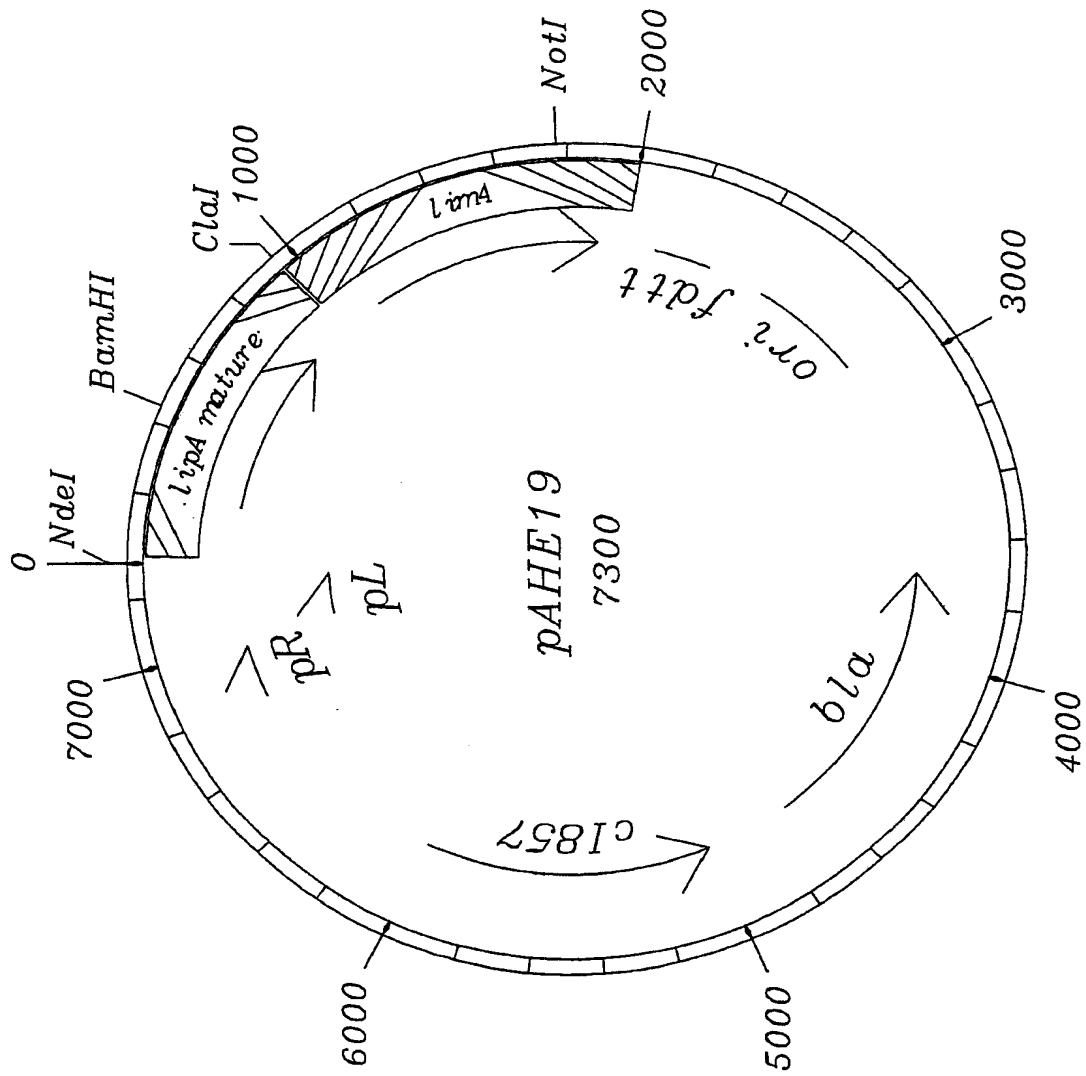


Fig. 12

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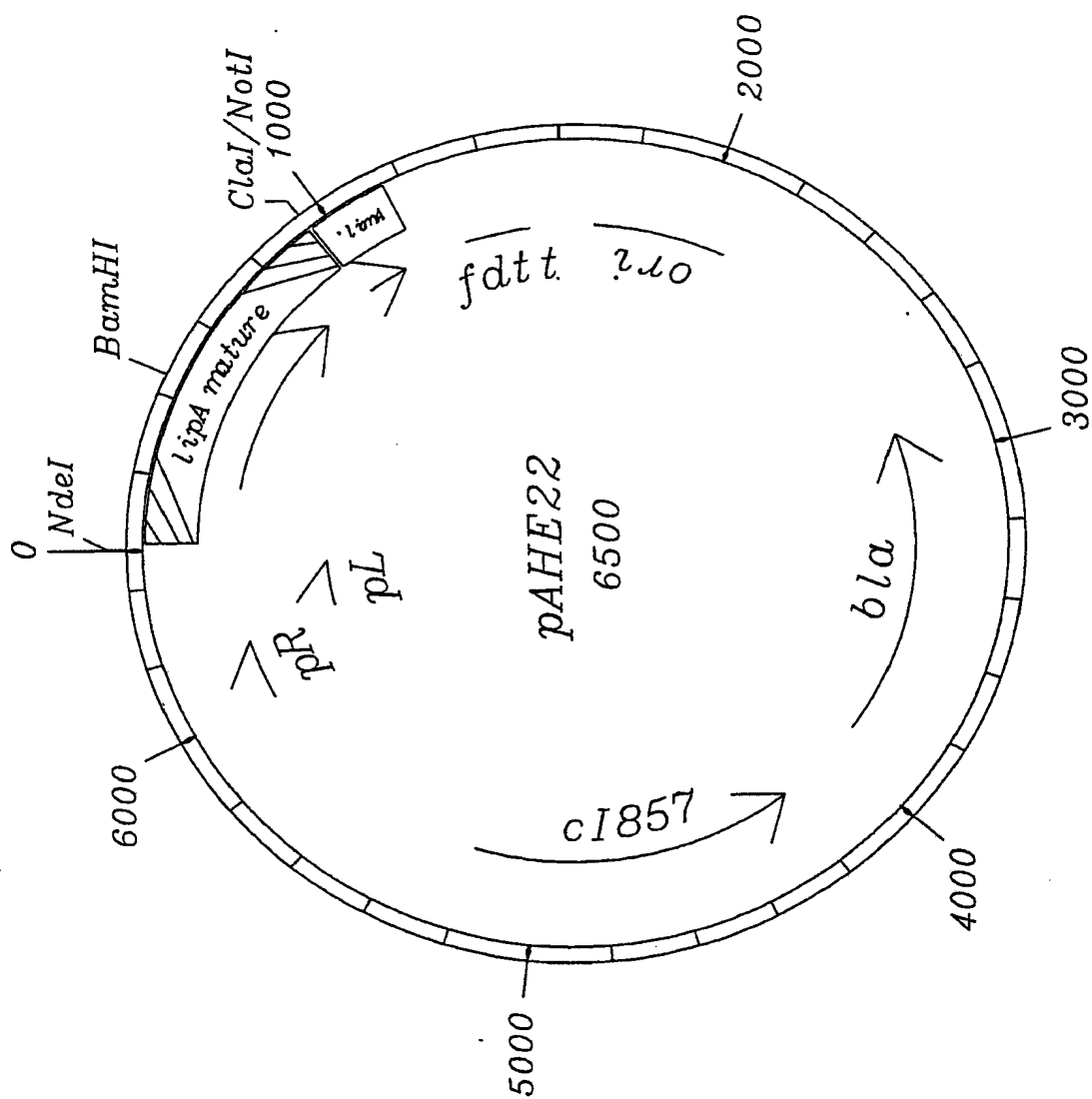


Fig. 13

SUBSTITUTE SHEET

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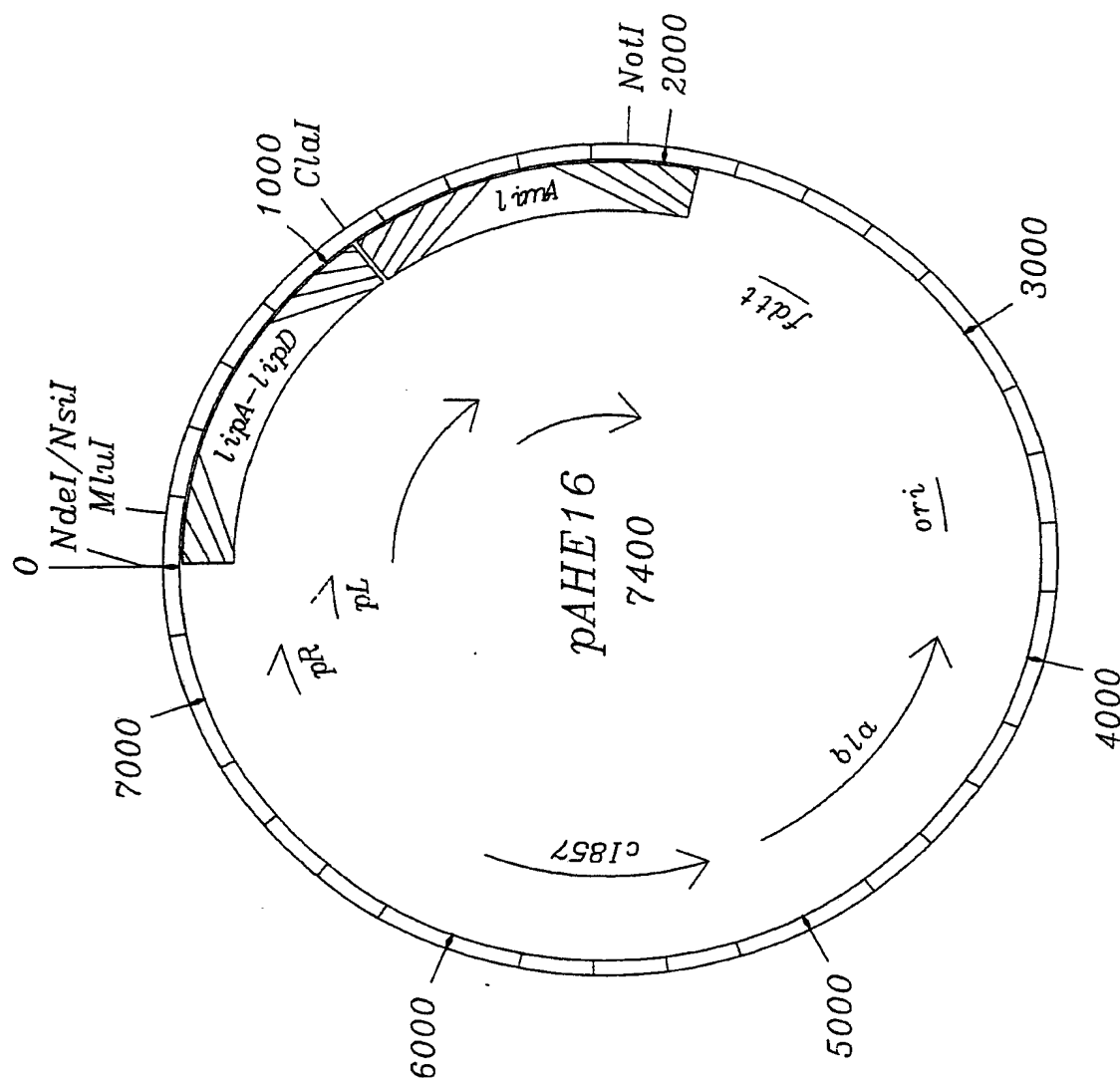


Fig. 14

SUBSTITUTE SHEET

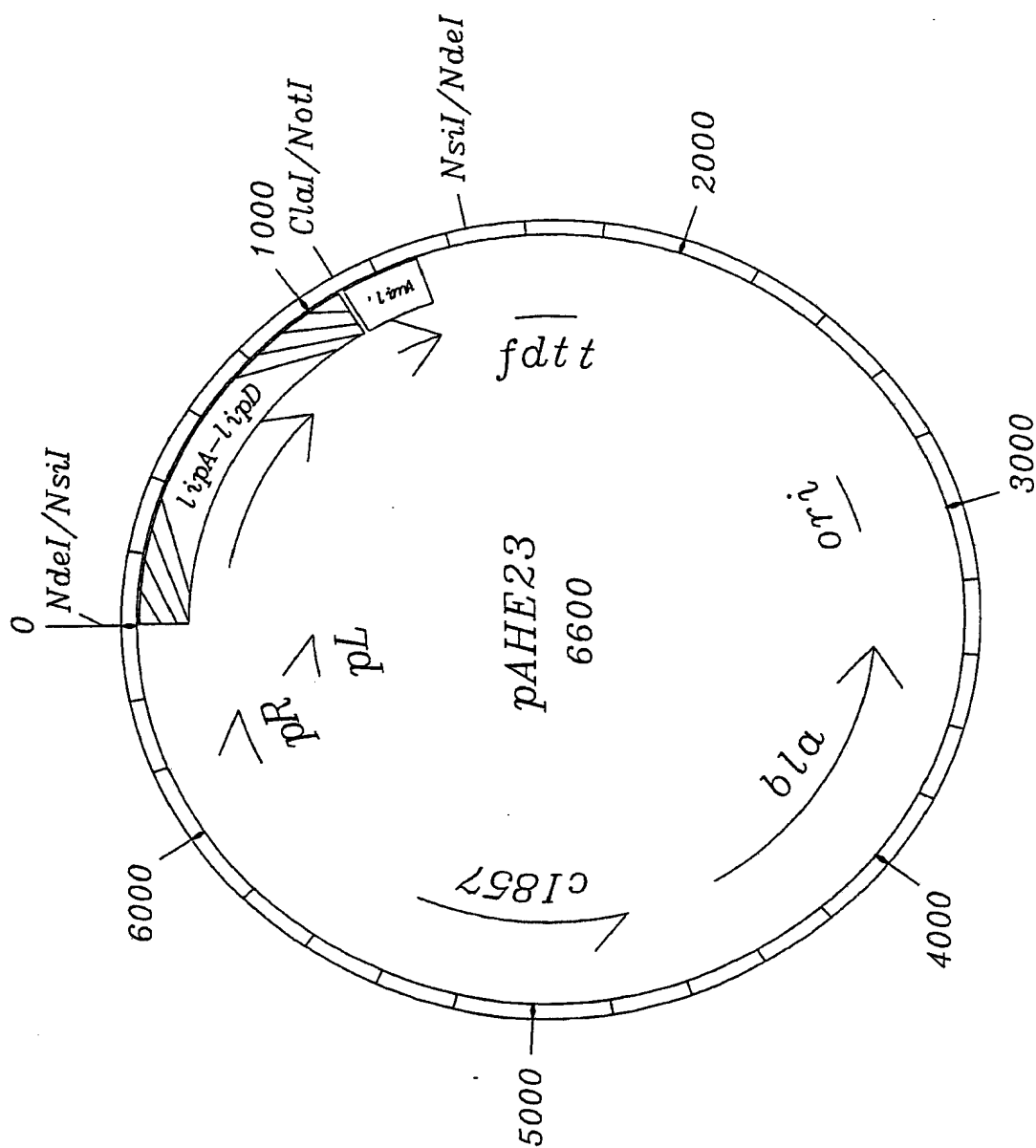


Fig. 15

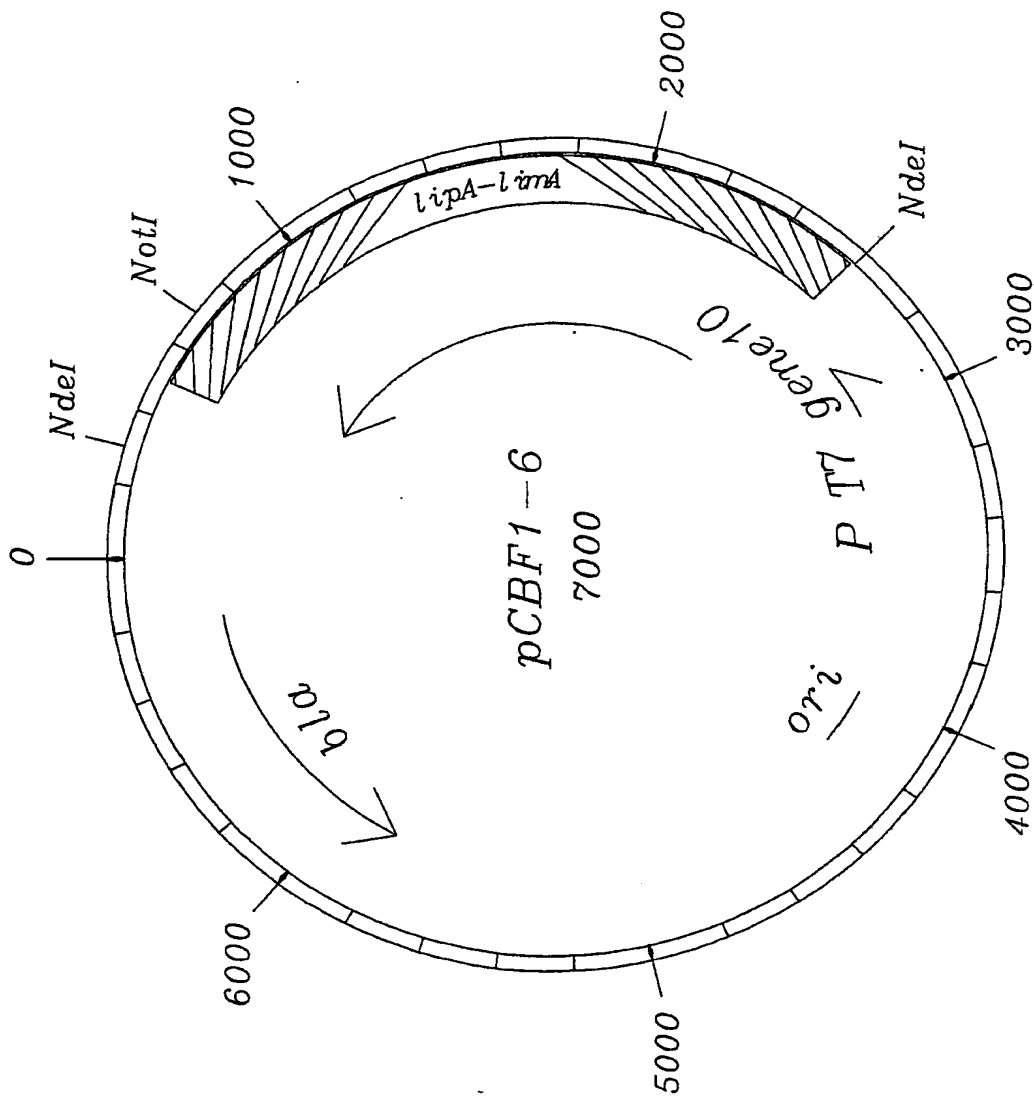


Fig. 16

1
INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 92/00391

A. CLASSIFICATION OF SUBJECT MATTER

IPC5: C12N 9/20, C12N 15/67, C12N 15/55, C12N 15/62
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC5: C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SE,DK,FI,NO classes as above

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

WPI, CA, MEDLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	EP, A1, 0464922 (UNILEVER NV ET AL.), 8 January 1992 (08.01.92), see page 3 lines 14-23, page 4 lines 15-26 --	5-14,18-30
X	Journal of Bacteriology, Volume 173, No 2, January 1991, Steen Jorgensen et al., "Cloning, Sequence, and Expression of a Lipase Gene from Pseudomonas cepacia: Lipase Production in Heterologous Hosts Requires Two Pseudomonas Genes", see discussion pages 565-566 --	5-14,18-30
X	WO, A1, 100908 (NOVO NORDISK A/S), 24 January 1991 (24.01.91), see page 3 lines 16-31 and the claims	5-14,18-30
A	--	1-4,15-17

☒ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

- * Special categories of cited documents:
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 - "O" document referring to an oral disclosure, use, exhibition or other means
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- "Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
- "&" document member of the same patent family

Date of the actual completion of the international search

Date of mailing of the international search report

25 March 1993

05 -04- 1993

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 92/00391

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	EP, A2, 0331376 (AMANO PHARMACEUTICAL CO., LTD.), 6 Sept 1989 (06.09.89) --	1-30
A	Chemical Abstracts, Volume 111, No 21, 20 November 1989 (20.11.89), (Columbus, Ohio, USA), Ellis R. John et al., "Molecular chaperones: proteins essential for the biogenesis of some macromolecular structures", page 294, THE ABSTRACT No 189647r, Trends Biochem. Sci. (Pers. Ed.) 1989, 14 (8), 339-342, (e) -- -----	1-30

INTERNATIONAL SEARCH REPORT
Information on patent family members

26/02/93

International application No.
PCT/DK 92/00391

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
EP-A1-	0464922	08/01/92	CA-A-	2046249	07/01/92
WO-A1-	100908	24/01/91	NONE		
EP-A2-	0331376	06/09/89	JP-A-	3087187	11/04/91